GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 13:10:50 ; Search time 5974 Seconds
(without alignments)
11168.870 Million cell updates/sec

Title: US-10-811-170-1
Perfect score: 1377
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1377	100.0	1377	6	AX056749	AX056749 Sequence
2	1328.4	96.5	1453	6	AX056745	AX056745 Sequence
3	1049.2	76.2	1444	6	AX056747	AX056747 Sequence
4	1039	75.5	1359	6	AX056739	AX056739 Sequence
5	1032.4	75.0	1389	6	AX056741	AX056741 Sequence
6	987.4	71.7	1674	6	AX056737	AX056737 Sequence
7	982.4	71.3	1704	6	AX056743	AX056743 Sequence
8	980.8	71.2	1704	6	AX056735	AX056735 Sequence
9	687.2	49.9	1383	6	AX338526	AX338526 Sequence
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12	684	49.7	762	6	AX556168	AX556168 Sequence
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ALIGNMENTS

RESULT 1
AX056749
LOCUS AX056749 1377 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 15 from Patent WO0075319.
ACCESSION AX056749
VERSION AX056749.1 GI:12309728
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE Modified chimeric polypeptides with improved pharmacokinetic properties
JOURNAL Patent: WO 0075319-A 15 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1377; DB 6; Length 1377;
Best Local Similarity 100.0%; Pred. No. 6.2e-310;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
AX056745
LOCUS       AX056745               1453 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 11 from Patent WO0075319.
ACCESSION   AX056745
VERSION     AX056745.1  GI:12309724
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
  TITLE     Modified chimeric polypeptides with improved pharmacokinetic
            properties
  JOURNAL   Patent: WO 0075319-A 11 14-DEC-2000;
            REGENERON PHARMACEUTICALS, INC. (US)
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ORIGIN

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Qy      1372 AAATGA 1377
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RESULT 3
AX056747
LOCUS AX056747 1444 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 13 from Patent WO0075319.
ACCESSION AX056747
VERSION AX056747.1 GI:12309726
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE Modified chimeric polypeptides with improved pharmacokinetic properties
JOURNAL Patent: WO 0075319-A 13 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
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ORIGIN

Query Match 76.2%; Score 1049.2; DB 6; Length 1444;
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Matches 1201; Conservative 0; Mismatches 158; Indels 27; Gaps 3;

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Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
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Db        360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              |||||||||||||||||||||||||| |     |||   ||      |     | || ||
Db        420 CATCGACAAACCAATACAATCATAGATATCCAGCTGTTGCCCAGGAAGTCGCTGGAGCTG 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              || || || ||||| ||| | || || || |   |  ||||  | ||    ||  |
Db        480 CTGGTAGGGGAGAAGCTGGTCCTCAACTGCACCGTGTGGGCTGAGTTTAACTCAGGTGTC 539

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              |||  ||||||| |||||       | ||    |||      ||    ||   |
Db        540 ACCTTTGACTGGGACTACCCAGGGAAGCAGGCAGAGCGGGGTAAGTGGGTGCCCGAGCGA 599

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              |       ||| |   | |          || | |  |||| | | || ||  |
Db        600 CGCTCCCAACAGACCCACACAG---------AACTCTCCAGCATCCTGACCATCCACAAC 650

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              || | || |   ||||  || | |||    ||    ||  ||  ||  |   |
Db        651 GTCAGCCAGCACGACCTGGGCTCGTATGTGTGCAAGGCCAACAACGGCATCCAGCGATTT 710

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAA---------GGACAAAACTCACACATGC 711
              | | |||||    ||||  || ||||||||          ||||||||||||||||||
Db        711 CGGGAGAGCACCGAGGTCATTGTGCATGAAAATGGCCCGGGCGACAAAACTCACACATGC 770

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 830

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 890

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        891 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 950

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        951 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1010

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1011 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1070

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1071 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1130

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1190

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1250

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1310

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1370

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1430

Qy       1372 AAATGA 1377
              ||||||
Db       1431 AAATGA 1436


RESULT 4
AX056739
LOCUS       AX056739                1359 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 5 from Patent WO0075319.
ACCESSION   AX056739
VERSION     AX056739.1  GI:12309718
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
  TITLE     Modified chimeric polypeptides with improved pharmacokinetic
            properties
  JOURNAL   Patent: WO 0075319-A 5 14-DEC-2000;
            REGENERON PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .1359
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     CDS             1. .1359
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                     APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
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                     GK"
ORIGIN

  Query Match             75.5%;  Score 1039;  DB 6;  Length 1359;
  Best Local Similarity   86.3%;  Pred. No. 3.4e-231;
  Matches 1189;  Conservative    0;  Mismatches  170;  Indels   18;  Gaps    3;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||          ||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 111

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 171

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 231

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 291

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 351

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
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Db        352 CATCGACAAACCAATACAATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTA 411

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Db        412 CTTAGAGGCCATACTCTTGTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTT 471

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Db        472 CAAATGACCTGGAGTTACCCTGATGAAATTGACCAAAGCAATTCCCATGCCAACATATTC 531

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Db        532 TACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGT 591

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Db        592 GTAA---GGAGTGGACCATCATTCAAATCTGTTAACACCTC------AGTGCATATATAT 642

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Db        643 GATAAAGCAGGCCCGGGCGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 702

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Db        703 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 762

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Db        763 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 822

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Db        823 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 882

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Db        883 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 942

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Db        943 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1002

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Db       1003 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1062

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Db       1063 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1122

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Db       1123 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1182

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Db       1183 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1242

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Db       1243 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1302

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377

Db       1303 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1359


RESULT 5
AX056741
LOCUS       AX056741               1389 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 7 from Patent WO0075319.
ACCESSION   AX056741
VERSION     AX056741.1  GI:12309720
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
  TITLE     Modified chimeric polypeptides with improved pharmacokinetic
            properties
  JOURNAL   Patent: WO 0075319-A 7 14-DEC-2000;
            REGENERON PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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     CDS             1. .1389
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                     /protein_id="CAC22375.1"
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                     WSYPDEKNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVN
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                     KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI
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                     YTQKSLSLSPGK"
ORIGIN

  Query Match           75.0%;  Score 1032.4;  DB 6;  Length 1389;
  Best Local Similarity  85.5%;  Pred. No. 1.2e-229;
  Matches 1201;  Conservative    0;  Mismatches  161;  Indels   42;  Gaps    3;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Db         61 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 111

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Db        112 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 171

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Db        172 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 231

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Db        232 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 291

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Db        292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 351

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Db        352 CATCGACAAACCAATACAATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTA 411

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Db        412 CTTAGAGGCCATACTCTTGTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTT 471

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Db        472 CAAATGACCTGGAGTTACCCT------GATGAAAAAAATAAGAGAGCTTCCGTAAGGCGA 525
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Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
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Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
Db        586 ATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAA 645

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAA----------------------------G 693
Db        646 TCTGTTAACACCTCAGTGCATATATATGATAAAGCAGGCCCGGGCGAGCCCAAATCTTGT 705

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
Db        706 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 765

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
Db        766 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 825

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
Db        826 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 885

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
Db        886 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 945

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
Db        946 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 1005

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
Db       1006 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1065

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
Db       1066 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1125

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
Db       1246 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1305

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
Db       1306 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1365

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
Db       1366 CTCTCCCTGTCTCCGGGTAAATGA 1389
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RESULT 6
AX056737
LOCUS       AX056737               1674 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 3 from Patent WO0075319.
ACCESSION   AX056737
VERSION     AX056737.1  GI:12309716
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
  TITLE     Modified chimeric polypeptides with improved pharmacokinetic
            properties
  JOURNAL   Patent: WO 0075319-A 3 14-DEC-2000;
            REGENERON PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .1674
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                     TSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKT
                     NYLTHRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEIDQSN
                     SHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTH
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                     EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                     GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
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ORIGIN
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  Query Match           71.7%;  Score 987.4;  DB 6;  Length 1674;
  Best Local Similarity  86.1%;  Pred. No. 3.6e-219;
  Matches 1119;  Conservative    0;  Mismatches  171;  Indels    9;  Gaps    2;

Qy         79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138
Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258
Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318
Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378
Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438
Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498
Db        745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy        499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558
Db        805 CCTGATGAAATTGACCAAAGCAATTCCCATGCCAACATATTCTACAGTGTTCTTACTATT 864

Qy        559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618
Db        865 GACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAA---GGAGTGGACCA 921

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678
Db        922 TCATTCAAATCTGTTAACACCTC------AGTGCATATATATGATAAAGCAGGCCCGGGC 975

Qy        679 AGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 738
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Db        976 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 1035

Qy        739 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 798
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Db       1036 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 1095

Qy        799 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 858
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Db       1096 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 1155

Qy        859 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 918
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Db       1156 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 1215

Qy        919 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 978
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Db       1216 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1275

Qy        979 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1335

Qy       1039 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1395

Qy       1099 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1455

Qy       1159 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1218
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Db       1456 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1515

Qy       1219 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1278
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Db       1516 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1575

Qy       1279 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1635

Qy       1339 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
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Db       1636 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1674


RESULT 7
AX056743
LOCUS       AX056743                1704 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 9 from Patent WO0075319.
ACCESSION   AX056743
VERSION     AX056743.1  GI:12309722
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
  TITLE     Modified chimeric polypeptides with improved pharmacokinetic
            properties
  JOURNAL   Patent: WO 0075319-A 9 14-DEC-2000;
            REGENERON PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
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     CDS             1..1704
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                     SVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGP
                     GEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
                     VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
                     PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
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                     K"
ORIGIN

  Query Match             71.3%;  Score 982.4;  DB 6;  Length 1704;
  Best Local Similarity   85.4%;  Pred. No. 5.3e-218;
  Matches 1132;  Conservative    0;  Mismatches  161;  Indels   33;  Gaps    2;

Qy         79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138
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Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
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Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258
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Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318
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Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378
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Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438
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Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498
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Db        745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy        499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558
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Db        805 CCTGATGAAAAAAATAAGAACGCTTCCGTAAGGCGACGAATTGACCAAAGCAATTC---- 860

Qy        559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618
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Db        861 --CCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAA 918

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678
              ||| | || || |||   | |   ||||| |       |||       | ||| |  ||
Db        919 GGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAATCTGTTAACACCTCAGTG 978

Qy        679 AGGGTCCATGAAAA---------------------------GGACAAAACTCACACATGC 711
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Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
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Db       1039 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 1098

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
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Db       1099 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 1158

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
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Db       1159 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 1218
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Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
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Db       1219 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1278

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
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Db       1279 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1338

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
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Db       1339 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1398

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
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Db       1399 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1458

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1518

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1578

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
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Db       1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1638

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1698

Qy       1372 AAATGA 1377
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Db       1699 AAATGA 1704
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RESULT 8
AX056735
LOCUS AX056735 1704 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 1 from Patent WO0075319.
ACCESSION AX056735
VERSION AX056735.1 GI:12309714
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE Modified chimeric polypeptides with improved pharmacokinetic properties
JOURNAL Patent: WO 0075319-A 1 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1. .1704
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CDS 1. .1704
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/db_xref="GI:12309715"
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PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
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ORIGIN

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Query Match            71.2%;  Score 980.8;  DB 6;  Length 1704;
Best Local Similarity  85.3%;  Pred. No. 1.2e-217;
Matches 1131;  Conservative    0;  Mismatches  162;  Indels   33;  Gaps    2;

Qy         79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138
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Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
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Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258
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Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318
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Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378
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Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438
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Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498
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Db        859 TCCCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAA 918

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678
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Db        919 GGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAATCTGTTAACACCTCAGTG 978

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Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
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Db       1159 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 1218

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
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Db       1219 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1278

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
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Db       1279 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1338
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Qy       1012 GCCCTCCCAGCCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCCGAGAACCA 1071
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Db       1339 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCCGAGAACCA 1398

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
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Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
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Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
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Db       1519 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1578

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
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Db       1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1638

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
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Db       1639 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1698

Qy       1372 AAATGA 1377
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Db       1699 AAATGA 1704
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RESULT 9
AX338526
LOCUS       AX338526               1383 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 17 from Patent WO0185789.
ACCESSION   AX338526
VERSION     AX338526.1  GI:18128935
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Roczniak,S., Dubois-Stringfellow,N.A. and Zolotorev,A.
  TITLE     Method of regulating angiogenesis using ryk protein
  JOURNAL   Patent: WO 0185789-A 17 15-NOV-2001;
            Bayer Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             49.9%;  Score 687.2;  DB 6;  Length 1383;
  Best Local Similarity   99.6%;  Pred. No. 3.1e-149;
  Matches  689;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        686 ATGAAAAGGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGAC 745
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Db        692 ATGATGATGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGAC 751

Qy        746 CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTG 805
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Db        812 AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT 871

Qy        866 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA 931

Qy        926 GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 991

Qy        986 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1045
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        992 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1051

Qy       1046 AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC 1105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC 1111

Qy       1106 TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1112 TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG 1171

Qy       1166 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1172 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC 1231

Qy       1226 TGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC 1285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1232 TGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC 1291

Qy       1286 AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC 1345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1292 AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC 1351

Qy       1346 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
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Db       1352 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1383
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RESULT 10
AR112718
LOCUS       AR112718               2043 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 14 from patent US 6130202.
ACCESSION   AR112718
VERSION     AR112718.1  GI:14092618
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2043)
  AUTHORS   Greve,J.M. and McClelland,A.
  TITLE     Antiviral methods
  JOURNAL   Patent: US 6130202-A 14 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .2043
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             49.8%;  Score 686;  DB 6;  Length 2043;
  Best Local Similarity   95.9%;  Pred. No. 6e-149;
  Matches  704;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy        644 GTGGGCTGATGACCAAGAAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTC 703
              | | | | |    ||||  || |   |   | ||      ||   |  ||||||||||||
Db       1310 GGGAGGTCACCCGCAAGGTGACCGTGAATGTGCTCTCCCCCCGGTATGAGGACAAAACTC 1369

Qy        704 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1370 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 1429

Qy        764 CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1430 CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 1489

Qy        824 TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1490 TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 1549

Qy        884 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA 943
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Db       1550 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCA 1609

Qy        944 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1610 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 1669

Qy       1004 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1670 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1729

Qy       1064 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 1123
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Db       1730 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 1789

Qy       1124 GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA 1183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1790 GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA 1849

Qy       1184 ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCT 1243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1850 ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCT 1909

Qy       1244 TCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCT 1303
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Db       1910 TCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCT 1969

Qy       1304 CATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGT 1363
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Db       1970 CATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGT 2029

Qy       1364 CTCCGGGTAAATGA 1377
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Db       2030 CTCCGGGTAAATGA 2043
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RESULT 11
AR380678
LOCUS AR380678 705 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1223 from patent US 6607879.
ACCESSION AR380678
VERSION AR380678.1 GI:40088312
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 705)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 1223 19-AUG-2003;
FEATURES Location/Qualifiers
source 1. .705
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 49.7%; Score 684; DB 6; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 64

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 124

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 184

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 244

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 304

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 364

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 424

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 484

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 544

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 604

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 664

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||
Db        665 CTCTCCCTGTCTCCGGGTAAATGA 688
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RESULT 12
AX556168
LOCUS AX556168 762 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 17 from Patent WO0238766.
ACCESSION AX556168
VERSION AX556168.1 GI:25899545
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gross,J.A., Xu,W., Henne,R.M. and Grant,F.J.
TITLE Human tumor necrosis factor receptor
JOURNAL Patent: WO 0238766-A 17 16-MAY-2002;
ZymoGenetics, Inc. (US)
FEATURES Location/Qualifiers
source 1. .762
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
CDS 7. .762
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD58267.1"
/db_xref="GI:25899546"
/translation="MKHLWFFLLLVAAPRWVLSEPKSCDKTHTCPPCPAPELLGGPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK"
ORIGIN

Query Match 49.7%; Score 684; DB 6; Length 762;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 138

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 198

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 258

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 318

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        319 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 378

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 438

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 498

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 558

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 618

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        619 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 678

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 738

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        739 CTCTCCCTGTCTCCGGGTAAATGA 762
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RESULT 13
AR137115
LOCUS       AR137115               1019 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6197294.
ACCESSION   AR137115
VERSION     AR137115.1  GI:14478624
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   Tao,W., Wong,S., Hickey,W.F., Hammang,J.P. and Baetge,E.Edward.
  TITLE     Cell surface molecule-induced macrophage activation
  JOURNAL   Patent: US 6197294-A 1 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .1019
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             49.7%;  Score 684;  DB 6;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-148;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db        328 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 387

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 447

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        448 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 507

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        508 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 567

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        568 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 627

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        628 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 687

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Db        688 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 747

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db        748 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 807

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        808 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 867

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        868 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 927

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 987

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        988 CTCTCCCTGTCTCCGGGTAAATGA 1011
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RESULT 14
BD271954
LOCUS       BD271954               1019 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Cell surface molecule-induced macrophage activation.
ACCESSION   BD271954
VERSION     BD271954.1  GI:33081722
KEYWORDS    JP 2002528078-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   Tao,W., Wong,S., Hickey,W.F., Hammang,J.P. and Baetge,E.E.
  TITLE     Cell surface molecule-induced macrophage activation
  JOURNAL   Patent: JP 2002528078-A 1 03-SEP-2002;
            NEUROTECH SA
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002528078-A/1
            PD   03-SEP-2002
            PF   21-OCT-1999 JP 2000578449
            PR   26-OCT-1998 US    09/178869
            PI   WENG TAO,SHOU WONG,WILLIAM F HICKEY,JOSEPH P HAMMANG,EDWARD E
            PI   BAETGE
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              A61P1/16,
            PC   A61P3/10,A61P7/06,A61P9/02,A61P11/02,A61P11/06,A61P17/00, PC
            A61P17/06,
            PC   A61P19/02,A61P21/02,A61P21/04,A61P25/00,A61P35/00,A61P37/02,
            PC   A61P37/06,
            PC   C07K14/705,C07K16/46,C07K19/00,C12N5/10,C12N15/00,C12N5/00, PC
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                      Location/Qualifiers
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FEATURES             Location/Qualifiers
     source          1. .1019
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ORIGIN

  Query Match            49.7%;  Score 684;  DB 6;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-148;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db        328 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 387

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 567

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        568 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 627

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        628 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 687

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db         988 CTCTCCCTGTCTCCGGGTAAATGA 1011


RESULT 15
AR275187
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LOCUS       AR275187               1019 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6506891.
ACCESSION   AR275187
VERSION     AR275187.1  GI:29708174
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   Tao,W., Wong,S., Hickey,W.F., Hammang,J.P. and Baetge,E.E.
  TITLE     Cell surface molecule-induced macrophage activation
  JOURNAL   Patent: US 6506891-A 1 14-JAN-2003;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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ORIGIN

  Query Match            49.7%;  Score 684;  DB 6;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-148;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db        328 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 387

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 447

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 507

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 567

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        568 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 627

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        628 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 687

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 747

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db         748 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 807

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db         988 CTCTCCCTGTCTCCGGGTAAATGA 1011


Search completed: September 23, 2005, 15:40:24
Job time : 5983 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1377	100.0	1377	5	AAA91076	Aaa91076 Flt1 rece
2	1377	100.0	1377	6	ABQ74610	Abq74610 Modified
3	1328.4	96.5	1453	5	AAA91074	Aaa91074 Flt1 rece
4	1328.4	96.5	1453	6	ABQ74608	Abq74608 Modified
5	1049.2	76.2	1444	5	AAA91075	Aaa91075 Flt1 rece
6	1049.2	76.2	1444	6	ABQ74609	Abq74609 Modified
7	1039	75.5	1359	5	AAA91071	Aaa91071 Flt1 rece
8	1039	75.5	1359	6	ABQ74605	Abq74605 Mutation
9	1032.4	75.0	1389	5	AAA91072	Aaa91072 Flt1 rece
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12	987.4	71.7	1674	6	ABQ74604	Abq74604 Mutation
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14	982.4	71.3	1704	6	ABQ74607	Abq74607 Mutation
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16	980.8	71.2	1704	6	ABQ74603	Abq74603 Flt1(1-3)
17	687.8	49.9	1290	10	AAL56122	Aal56122 Plasmid p
18	687.8	49.9	1290	12	ADO10510	Ado10510 Kb/EPO/Ig
19	687.8	49.9	1299	10	AAL56123	Aal56123 Plasmid p
20	687.8	49.9	1299	12	ADO10512	Ado10512 EPO/IgG1
21	687.2	49.9	1383	6	AAI67766	Aai67766 Human Ryk
22	687.2	49.9	1389	10	ADC98597	Adc98597 Human ang
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25	687.2	49.9	1947	10	ADC98589	Adc98589 Human ang
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31	686	49.8	2043	2	AAQ55340	Aaq55340 tICAM(453
32	685.2	49.8	798	10	AAL56121	Aal56121 Plasmid p
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34	685	49.7	6097	5	AAF57869	Aaf57869 OPG-Fc co
35	684	49.7	705	11	ADI31897	Adi31897 Human cDN
36	684	49.7	705	12	ADL46173	Adl46173 Human imm
37	684	49.7	762	6	ABN89435	Abn89435 Human imm
38	684	49.7	762	10	AAD53735	Aad53735 Human wil
39	684	49.7	762	10	AAD53755	Aad53755 Human mod
40	684	49.7	762	10	AAD53760	Aad53760 Human mod
41	684	49.7	993	12	ADM68909	Adm68909 Human IgG
42	684	49.7	1002	12	ADL22760	Adl22760 Human ant
43	684	49.7	1002	12	ADN97484	Adn97484 Artificia
44	684	49.7	1019	3	AAA53126	Aaa53126 Human TR-
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ALIGNMENTS

RESULT 1
AAA91076
ID AAA91076 standard; DNA; 1377 BP.
XX
AC AAA91076;
XX
DT 05-APR-2001 (first entry)
XX
DE Flt1 receptor fusion protein VEGFR1R2-FcDeltaC2 (a) coding sequence.
XX
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .1377
FT /*tag= a
FT /product= "VEGFR1R2-FcDeltaC2(a)"
XX
PN WO200075319-A1.
XX
PD 14-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US014142.
XX
PR 08-JUN-1999; 99US-0138133P.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Papadopoulos NJ, Davis S, Yancopoulos GD;
XX
DR WPI; 2001-071076/08.
DR P-PSDB; AAY97596.
XX
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model
PT systems.
XX
PS Claim 9; Fig 24; 159pp; English.
XX
CC This sequence encodes a fusion protein of the invention between the Flt1

```
CC   receptor and the Fc region of IgG. The specification relates to modified
CC   chimeric polypeptides with improved pharmacokinetics. The modified
CC   chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC   been modified to improve their pharmacokinetic profile. The polypeptides
CC   can be used to decrease or inhibit plasma leakage and/or vascular
CC   permeability in a mammal
XX
SQ   Sequence 1377 BP; 386 A; 374 C; 339 G; 278 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1377;  DB 5;  Length 1377;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
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Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
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Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
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Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
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Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
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Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
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Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
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Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
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Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
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Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
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Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

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Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
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Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
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Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
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Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
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Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
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Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
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Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
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Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377


RESULT 2
ABQ74610
ID   ABQ74610 standard; cDNA; 1377 BP.
XX
AC   ABQ74610;
XX
DT   23-OCT-2002  (first entry)
XX
DE   Modified Flt1 receptor VEGFR1R2-FcDELTAC1(a) nucleotide sequence.
XX
KW   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW   psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW   vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW   ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW   brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW   kidney disease; eye disorder; age-related macular degeneration;
KW   diabetic retinopathy; gene; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1377
FT                   /*tag=  a
FT                   /product= "VEGFR1R2-FcDELTAC1(a)"
XX
PN   WO200260489-A1.
XX
PD   08-AUG-2002.
XX
PF   28-JAN-2002; 2002WO-US002466.
XX
PR   31-JAN-2001; 2001US-00773877.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Xia Y,  Rudge JS,  Yancopoulos GD;
XX
DR   WPI; 2002-608488/65.
DR   P-PSDB; ABP52449.
```

```
XX
PT   Treating psoriasis and enhancing wound healing in humans comprises the
PT   administration of a vascular endothelial cell growth factor (VEGF)
PT   antagonist.
XX
PS   Example 20; Fig 24A-C; 179pp; English.
XX
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence encodes VEGFR1R2-
CC   FcDELTAC1(a) which is used in an example from the present invention
XX
SQ   Sequence 1377 BP; 386 A; 374 C; 339 G; 278 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1377;  DB 6;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377


RESULT 3
AAA91074
ID   AAA91074 standard; DNA; 1453 BP.
XX
AC   AAA91074;
XX
DT   05-APR-2001  (first entry)
XX
DE   Flt1 receptor fusion protein Flt1D2.Flk1D3:FcDeltaC1(a) coding sequence.
XX
KW   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW   plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS   Unidentified.
XX
PN   WO200075319-A1.
XX
PD   14-DEC-2000.
XX
PF   23-MAY-2000; 2000WO-US014142.
XX
PR   08-JUN-1999;   99US-0138133P.
XX
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PA   (REGE-) REGENERON PHARM INC.
XX
PI   Papadopoulos NJ,  Davis S,  Yancopoulos GD;
XX
DR   WPI; 2001-071076/08.
DR   .P-PSDB; AAY97594.
XX
PT   Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT   and its fragments, useful for diagnosis, evaluation, and treatment of
PT   diseases associated with the gene expression and for producing model
PT   systems.
XX
PS   Claim 9; Fig 21; 159pp; English.
XX
CC   This sequence encodes a fusion protein of the invention between the Flt1
CC   receptor and the Fc region of IgG. The specification relates to modified
CC   chimeric polypeptides with improved pharmacokinetics. The modified
CC   chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC   been modified to improve their pharmacokinetic profile. The polypeptides
CC   can be used to decrease or inhibit plasma leakage and/or vascular
CC   permeability in a mammal
XX
SQ   Sequence 1453 BP; 398 A; 400 C; 366 G; 289 T; 0 U; 0 Other;

  Query Match             96.5%;  Score 1328.4;  DB 5;  Length 1453;
  Best Local Similarity   98.6%;  Pred. No. 3e-312;
  Matches 1367;  Conservative    0;  Mismatches    1;  Indels   18;  Gaps    2;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||          ||||||||||||||||||||||||||||||||||
Db        129 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 179

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 239

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 299

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 359

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 539

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 599

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 659

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAG---------GACAAAACTCACACATGC 711
              |||||||||||||||||||||||||||||||         |||||||||||||||||||
Db        720 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGGCCCGGGCGACAAAACTCACACATGC 779

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 839

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 899

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 959

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1019

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1079

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1080 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1139

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1199

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1259

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1319

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1379

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1439

Qy       1372 AAATGA 1377
              ||||||
Db       1440 AAATGA 1445


RESULT 4
ABQ74608
ID   ABQ74608 standard; cDNA; 1453 BP.
XX
AC   ABQ74608;
XX
DT   23-OCT-2002  (first entry)
XX
DE   Modified Flt1 receptor Flt1D2.Flk1D3.FcDELTAC1(a) nucleotide sequence.
XX
KW   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW   psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW   vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW   ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW   brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW   kidney disease; eye disorder; age-related macular degeneration;
KW   diabetic retinopathy; gene; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
```

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FH   Key             Location/Qualifiers
FT   CDS             69. .1445
FT                   /*tag= a
FT                   /product= "Flt1D2.Flk1D3.FcDELTAC1(a)"
XX
PN   WO200260489-A1.
XX
PD   08-AUG-2002.
XX
PF   28-JAN-2002; 2002WO-US002466.
XX
PR   31-JAN-2001; 2001US-00773877.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Xia Y,  Rudge JS,  Yancopoulos GD;
XX
DR   WPI; 2002-608488/65.
DR   P-PSDB; ABP52447.
XX
PT   Treating psoriasis and enhancing wound healing in humans comprises the
PT   administration of a vascular endothelial cell growth factor (VEGF)
PT   antagonist.
XX
PS   Example 17; Fig 21A-C; 179pp; English.
XX
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence encodes
CC   Flt1D2.Flk1D3.FcDELTAC1(a) which is used in an example from the present
CC   invention
XX
SQ   Sequence 1453 BP; 398 A; 400 C; 366 G; 289 T; 0 U; 0 Other;

  Query Match             96.5%;  Score 1328.4;  DB 6;  Length 1453;
  Best Local Similarity   98.6%;  Pred. No. 3e-312;
  Matches 1367;  Conservative    0;  Mismatches    1;  Indels   18;  Gaps    2;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||          ||||||||||||||||||||||||||||||
Db        129 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 179

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 239

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 299

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 359

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 539

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 599

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 659

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAG---------GACAAAACTCACACATGC 711
              ||||||||||||||||||||||||||||||||          ||||||||||||||||||
Db        720 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGGCCCGGGCGACAAAACTCACACATGC 779

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 839

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 899

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 959

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1019

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1079

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1080 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1139

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1199

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1259

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1319

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1379

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1439

Qy       1372 AAATGA 1377
              ||||||
Db       1440 AAATGA 1445
```

```
RESULT 5
AAA91075
ID   AAA91075 standard; DNA; 1444 BP.
XX
AC   AAA91075;
XX
DT   05-APR-2001  (first entry)
XX
DE   Flt1 receptor fusion protein Flt1D2.VEGFR3D3.fcDeltaC1(a) DNA sequence.
XX
KW   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW   plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS   Unidentified.
XX
PN   WO200075319-A1.
XX
PD   14-DEC-2000.
XX
PF   23-MAY-2000; 2000WO-US014142.
XX
PR   08-JUN-1999;   99US-0138133P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Papadopoulos NJ,  Davis S,  Yancopoulos GD;
XX
DR   WPI; 2001-071076/08.
DR   P-PSDB; AAY97595.
XX
PT   Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT   and its fragments, useful for diagnosis, evaluation, and treatment of
PT   diseases associated with the gene expression and for producing model
PT   systems.
XX
PS   Claim 9; Fig 22; 159pp; English.
XX
CC   This sequence encodes a fusion protein of the invention between the Flt1
CC   receptor and the Fc region of IgG. The specification relates to modified
CC   chimeric polypeptides with improved pharmacokinetics. The modified
CC   chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC   been modified to improve their pharmacokinetic profile. The polypeptides
CC   can be used to decrease or inhibit plasma leakage and/or vascular
CC   permeability in a mammal
XX
SQ   Sequence 1444 BP; 371 A; 426 C; 380 G; 267 T; 0 U; 0 Other;

  Query Match             76.2%;  Score 1049.2;  DB 5;  Length 1444;
  Best Local Similarity   86.7%;  Pred. No. 1.8e-244;
  Matches 1201;  Conservative    0;  Mismatches  158;  Indels   27;  Gaps    3;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||          ||||||||||||||||||||||||||||||||||
Db        129 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 179

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 239

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 299

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 359

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              |||||||||||||||||||||||||| |   |||   ||     |    | || ||
Db        420 CATCGACAAACCAATACAATCATAGATATCCAGCTGTTGCCCAGGAAGTCGCTGGAGCTG 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              || || || ||||| ||| | || || || |   |  |||| | ||    || |
Db        480 CTGGTAGGGGAGAAGCTGGTCCTCAACTGCACCGTGTGGGCTGAGTTTAACTCAGGTGTC 539

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              |||  ||||||| |||||      | ||    |||     ||   ||  |
Db        540 ACCTTTGACTGGGACTACCCAGGGAAGCAGGCAGAGCGGGGTAAGTGGGTGCCCGAGCGA 599

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              |     ||| |   | |          || | |  |||| | | || ||  |
Db        600 CGCTCCCAACAGACCCACACAG---------AACTCTCCAGCATCCTGACCATCCACAAC 650

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              || | ||  |   ||||  || | |||    ||    ||   ||  |   |
Db        651 GTCAGCCAGCACGACCTGGGCTCGTATGTGTGCAAGGCCAACAACGGCATCCAGCGATTT 710

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAA---------GGACAAAACTCACACATGC 711
              | | |||||    ||||  || ||||||||          |||||||||||||||||
Db        711 CGGGAGAGCACCGAGGTCATTGTGCATGAAAATGGCCCGGGCGACAAAACTCACACATGC 770

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 830

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 890

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        891 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 950

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        951 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1010

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1011 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1070

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1071 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1130

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1190

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1250

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1310

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1370

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1430

Qy       1372 AAATGA 1377
              ||||||
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Db       1431 AAATGA 1436


RESULT 6
ABQ74609
ID   ABQ74609 standard; cDNA; 1444 BP.
XX
AC   ABQ74609;
XX
DT   23-OCT-2002  (first entry)
XX
DE   Modified Flt1 receptor Flt1D2.VEGFR3D3.FcDELTAC1(a) nucleotide sequence.
XX
KW   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW   psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW   vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW   ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW   brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW   kidney disease; eye disorder; age-related macular degeneration;
KW   diabetic retinopathy; gene; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             69. .1436
FT                   /*tag=  a
FT                   /product= "Flt1D2.VEGFR3D3.FcDELTAC1(a)"
XX
PN   WO200260489-A1.
XX
PD   08-AUG-2002.
XX
PF   28-JAN-2002; 2002WO-US002466.
XX
PR   31-JAN-2001; 2001US-00773877.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Xia Y,  Rudge JS,  Yancopoulos GD;
XX
DR   WPI; 2002-608488/65.
DR   P-PSDB; ABP52448.
XX
PT   Treating psoriasis and enhancing wound healing in humans comprises the
PT   administration of a vascular endothelial cell growth factor (VEGF)
PT   antagonist.
XX
PS   Example 17; Fig 22A-C; 179pp; English.
XX
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence encodes
CC   Flt1D2.VEGFR3D3.FcDELTAC1(a) which is used in an example from the present
CC   invention
XX
SQ   Sequence 1444 BP; 371 A; 426 C; 380 G; 267 T; 0 U; 0 Other;

  Query Match            76.2%;  Score 1049.2;  DB 6;  Length 1444;
  Best Local Similarity  86.7%;  Pred. No. 1.8e-244;
  Matches 1201;  Conservative    0;  Mismatches  158;  Indels   27;  Gaps    3;
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```
Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||         ||||||||||||||||||||||||||||||||
Db        129 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 179

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 239

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 299

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 359

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              |||||||||||||||||||||||||| |    |||   ||     |     | || ||
Db        420 CATCGACAAACCAATACAATCATAGATATCCAGCTGTTGCCCAGGAAGTCGCTGGAGCTG 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              || || || ||||| ||| | || || || |   |  ||||  | ||    ||  |
Db        480 CTGGTAGGGGAGAAGCTGGTCCTCAACTGCACCGTGTGGGCTGAGTTTAACTCAGGTGTC 539

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              |||  |||||| |||||      | ||    |||     ||    ||   |
Db        540 ACCTTTGACTGGGACTACCCAGGGAAGCAGGCAGAGCGGGGTAAGTGGGTGCCCGAGCGA 599

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              |        ||| |    | |         || | |  |||| | | || ||  |
Db        600 CGCTCCCAACAGACCCACACAG---------AACTCTCCAGCATCCTGACCATCCACAAC 650

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              || | || |   |||| || | |||    ||    ||   ||  ||  |   |
Db        651 GTCAGCCAGCACGACCTGGGCTCGTATGTGTGCAAGGCCAACAACGGCATCCAGCGATTT 710

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAA---------GGACAAAACTCACACATGC 711
              | | |||||    |||| || ||||||||          ||||||||||||||||||
Db        711 CGGGAGAGCACCGAGGTCATTGTGCATGAAAATGGCCCGGGCGACAAAACTCACACATGC 770

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 830

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 890

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        891 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 950

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        951 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1010

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1011 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1070

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1071 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1130
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Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1190

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1250

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1310

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1370

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1430

Qy       1372 AAATGA 1377
             ||||||
Db       1431 AAATGA 1436
```

RESULT 7
AAA91071
ID AAA91071 standard; DNA; 1359 BP.
XX
AC AAA91071;
XX
DT 05-APR-2001 (first entry)
XX
DE Flt1 receptor fusion protein Mut2:Flt1(2-3deltaB)-Fc coding sequence.
XX
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .1359
FT /*tag= a
FT /product= "Flt1(2-3deltaB)-Fc"
XX
PN WO200075319-A1.
XX
PD 14-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US014142.
XX
PR 08-JUN-1999; 99US-0138133P.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Papadopoulos NJ, Davis S, Yancopoulos GD;
XX
DR WPI; 2001-071076/08.
DR P-PSDB; AAY97591.
XX
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model
PT systems.
XX
PS Claim 9; Fig 14; 159pp; English.
XX
CC This sequence encodes a fusion protein of the invention between the Flt1
CC receptor and the Fc region of IgG. The specification relates to modified
CC chimeric polypeptides with improved pharmacokinetics. The modified
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC been modified to improve their pharmacokinetic profile. The polypeptides
CC can be used to decrease or inhibit plasma leakage and/or vascular
CC permeability in a mammal
XX
SQ Sequence 1359 BP; 381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;

Query Match 75.5%; Score 1039; DB 5; Length 1359;
Best Local Similarity 86.3%; Pred. No. 5.3e-242;
Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;

```
Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              |||||||||||||||||          ||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 111

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 171

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 231

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 291

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 351

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||      | ||  |  | |    | |  || ||
Db        352 CATCGACAAACCAATACAATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTA 411

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
                |   ||  | |  |||||| | |||||||| || |  |||    | ||   | |  ||
Db        412 CTTAGAGGCCATACTCTTGTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTT 471

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              | | | ||||  ||||||  |  |  | ||   ||   | ||  |||  |  |
Db        472 CAAATGACCTGGAGTTACCCTGATGAAATTGACCAAAGCAATTCCCATGCCAACATATTC 531

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              |     |  ||       | ||| ||||       |      |  ||    | ||
Db        532 TACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGT 591

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||  ||||||  | |  ||| |  |  |    |  ||        ||   |  |
Db        592 GTAA---GGAGTGGACCATCATTCAAATCTGTTAACACCTC------AGTGCATATATAT 642

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              | ||          | |  |  | |       ||||||||||||||||||||||||||
Db        643 GATAAAGCAGGCCCGGGCGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 702

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 762

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 822

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        823 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 882

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 942

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1002

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1062

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1122

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1182

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1242

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1302

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1359
```

RESULT 8
ABQ74605
ID ABQ74605 standard; cDNA; 1359 BP.
XX
AC ABQ74605;
XX
DT 23-OCT-2002 (first entry)
XX
DE Mutation 2 Flt1(2-3 delta B)-Fc nucleotide sequence.
XX
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW kidney disease; eye disorder; age-related macular degeneration;
KW diabetic retinopathy; gene; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1359
FT   /*tag= a
FT   /product= "Mut2:Flt1(2-3 delta B)-Fc protein"
XX
PN WO200260489-A1.
XX
PD 08-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002466.
XX
PR 31-JAN-2001; 2001US-00773877.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Xia Y, Rudge JS, Yancopoulos GD;
XX
DR WPI; 2002-608488/65.
DR P-PSDB; ABP52444.
XX
PT Treating psoriasis and enhancing wound healing in humans comprises the
PT administration of a vascular endothelial cell growth factor (VEGF)
PT antagonist.
XX
PS Example 12; Fig 14A-C; 179pp; English.
XX
CC The present invention describes a method for treating psoriasis and
CC enhancing wound healing in a mammal or a human. The method comprises
CC administering a vascular endothelial cell growth factor (VEGF) antagonist
CC to the mammal or human. A VEGF antagonist has antipsoriatic,
CC antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC nephrotropic and ophthalmological activities. The method can be used in
CC treating psoriasis and enhancing wound healing in humans by administering
CC VEGF antagonist. The method is also useful in treating clinical
CC conditions characterised by vascular permeability, oedema or
CC inflammation, such as brain oedema associated with injury, oedema
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC asthma, burns, kidney diseases, or eye disorders such as age-related
CC macular degeneration and diabetic retinopathy. The method may also be
CC used in making the polypeptide to decrease or inhibit plasma leakage and
CC or vascular permeability. The present sequence encodes Mut2:Flt1(2-3
CC delta B)-Fc which is used in an example from the present invention
XX
SQ Sequence 1359 BP; 381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;

Query Match 75.5%; Score 1039; DB 6; Length 1359;
Best Local Similarity 86.3%; Pred. No. 5.3e-242;
Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;

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Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||         ||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 111

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 171

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 231

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 291

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 351

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||      | ||  |  | |    | |  || ||
Db        352 CATCGACAAACCAATACAATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTA 411

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              |  ||  | |  |||||| | |||||||| || |  |||    | ||   | |  ||
Db        412 CTTAGAGGCCATACTCTTGTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTT 471

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              |  | | ||||  ||||||  |   |  | ||    ||    | ||  |||  |  |
Db        472 CAAATGACCTGGAGTTACCCTGATGAAATTGACCAAAGCAATTCCCATGCCAACATATTC 531

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
                |      |  ||        | ||| ||||       |      |   ||    | ||
Db        532 TACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGT 591

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||   ||||||  | |  |||  | |   |   | ||      ||   |  |
Db        592 GTAA---GGAGTGGACCATCATTCAAATCTGTTAACACCTC------AGTGCATATATAT 642

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              | ||          | |  | | |       ||||||||||||||||||||||||||
Db        643 GATAAAGCAGGCCCGGGCGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 702
```

```
Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 762

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 822

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        823 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 882

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 942

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1002

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1062

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1122

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1182

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1242

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1302

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1359
```

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RESULT 9
AAA91072
ID   AAA91072 standard; DNA; 1389 BP.
XX
AC   AAA91072;
XX
DT   05-APR-2001  (first entry)
XX
DE   Flt1 receptor fusion protein Mut3:Flt1(2-3)-Fc coding sequence.
XX
KW   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW   plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1389
FT                   /*tag=  a
FT                   /product= "Flt1(2-3)-Fc"
XX
PN   WO200075319-A1.
XX
PD   14-DEC-2000.
XX
PF   23-MAY-2000; 2000WO-US014142.
XX
PR   08-JUN-1999;   99US-0138133P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Papadopoulos NJ,  Davis S,  Yancopoulos GD;
XX
DR   WPI; 2001-071076/08.
DR   P-PSDB; AAY97592.
XX
PT   Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT   and its fragments, useful for diagnosis, evaluation, and treatment of
PT   diseases associated with the gene expression and for producing model
PT   systems.
XX
PS   Claim 9; Fig 15; 159pp; English.
XX
CC   This sequence encodes a fusion protein of the invention between the Flt1
CC   receptor and the Fc region of IgG. The specification relates to modified
CC   chimeric polypeptides with improved pharmacokinetics. The modified
CC   chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC   been modified to improve their pharmacokinetic profile. The polypeptides
CC   can be used to decrease or inhibit plasma leakage and/or vascular
CC   permeability in a mammal
XX
SQ   Sequence 1389 BP; 394 A; 393 C; 322 G; 280 T; 0 U; 0 Other;
```

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  Query Match             75.0%;  Score 1032.4;  DB 5;  Length 1389;
  Best Local Similarity   85.5%;  Pred. No. 2.2e-240;
  Matches 1201;  Conservative    0;  Mismatches  161;  Indels   42;  Gaps    3;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              |||||||||||||||||          |||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 111

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 171

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 231

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 291

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 351

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||     | ||  |  | |    | |  || ||
Db        352 CATCGACAAACCAATACAATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTA 411

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
                |   ||  | |  |||||| | |||||||| || |  |||    | ||   | |  ||
Db        412 CTTAGAGGCCATACTCTTGTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTT 471

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              | | | ||||   ||||||       |  |  |  |||||| |  |       |
Db        472 CAAATGACCTGGAGTTACCCT------GATGAAAAAAATAAGAGAGCTTCCGTAAGGCGA 525

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              | ||   |||         |    || | ||| |  ||     | |||||  ||
Db        526 CGAATTGACCAAAGCAATTCCCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAA 585

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              |       |  ||| ||||| | || || |||   | |  |||||  |       |||
Db        586 ATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAA 645

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAA----------------------------G 693
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```
                    | ||| |  ||     |  |||| ||
Db        646 TCTGTTAACACCTCAGTGCATATATATGATAAAGCAGGCCCGGGCGAGCCCAAATCTTGT 705

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 765

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 825

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 885

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 945

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 1005

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1065

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1125

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1185

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1245

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1305

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1365

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
              |||||||||||||||||||||||||
Db       1366 CTCTCCCTGTCTCCGGGTAAATGA 1389
```

```
RESULT 10
ABQ74606
ID   ABQ74606 standard; cDNA; 1389 BP.
XX
AC   ABQ74606;
XX
DT   23-OCT-2002  (first entry)
XX
DE   Mutation 3 Flt1(2-3)-Fc nucleotide sequence.
XX
KW   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW   psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW   vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW   ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW   brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW   kidney disease; eye disorder; age-related macular degeneration;
KW   diabetic retinopathy; gene; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
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FH   Key             Location/Qualifiers
FT   CDS             1. .1389
FT                   /*tag=  a
FT                   /product= "Mut3:Flt1(2-3)-Fc protein"
XX
PN   WO200260489-A1.
XX
PD   08-AUG-2002.
XX
PF   28-JAN-2002; 2002WO-US002466.
XX
PR   31-JAN-2001; 2001US-00773877.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Xia Y,  Rudge JS,  Yancopoulos GD;
XX
DR   WPI; 2002-608488/65.
XX
PT   Treating psoriasis and enhancing wound healing in humans comprises the
PT   administration of a vascular endothelial cell growth factor (VEGF)
PT   antagonist.
XX
PS   Example 13; Fig 15A-C; 179pp; English.
XX
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence encodes Mut3:Flt1(2-3)-Fc
CC   which is used in an example from the present invention
XX
SQ   Sequence 1389 BP; 394 A; 393 C; 322 G; 280 T; 0 U; 0 Other;
```

```
  Query Match             75.0%;  Score 1032.4;  DB 6;  Length 1389;
  Best Local Similarity   85.5%;  Pred. No. 2.2e-240;
  Matches 1201;  Conservative    0;  Mismatches  161;  Indels   42;  Gaps    3;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              |||||||||||||||||          ||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 111

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 171

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 231

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 291

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 351

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
```

```
Db        352 CATCGACAAACCAATACAATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTA 411

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Db        412 CTTAGAGGCCATACTCTTGTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTT 471

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Db        472 CAAATGACCTGGAGTTACCCT------GATGAAAAAAATAAGAGAGCTTCCGTAAGGCGA 525

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Db        526 CGAATTGACCAAAGCAATTCCCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAA 585

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Db        586 ATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAA 645

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAA----------------------------G 693

Db        646 TCTGTTAACACCTCAGTGCATATATATGATAAAGCAGGCCCGGGCGAGCCCAAATCTTGT 705

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753

Db        706 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 765

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813

Db        766 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 825

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873

Db        826 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 885

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933

Db        886 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 945

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993

Db        946 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 1005

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053

Db       1006 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1065

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113

Db       1066 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1125

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173

Db       1126 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1185

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233

Db       1186 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1245

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293

Db       1246 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1305

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353

Db       1306 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1365

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377

Db       1366 CTCTCCCTGTCTCCGGGTAAATGA 1389
```

RESULT 11

```
AAA91070
ID   AAA91070 standard; DNA; 1674 BP.
XX
AC   AAA91070;
XX
DT   05-APR-2001  (first entry)
XX
DE   Flt1 receptor fusion protein Mut1:Flt1(1-3deltaB)-Fc coding sequence.
XX
KW   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW   plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1674
FT                   /*tag=  a
FT                   /product= "Flt1(1-3deltaB)-Fc"
XX
PN   WO200075319-A1.
XX
PD   14-DEC-2000.
XX
PF   23-MAY-2000; 2000WO-US014142.
XX
PR   08-JUN-1999;   99US-0138133P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Papadopoulos NJ,  Davis S,  Yancopoulos GD;
XX
DR   WPI; 2001-071076/08.
DR   P-PSDB; AAY97590.
XX
PT   Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT   and its fragments, useful for diagnosis, evaluation, and treatment of
PT   diseases associated with the gene expression and for producing model
PT   systems.
XX
PS   Claim 9; Fig 13; 159pp; English.
XX
CC   This sequence encodes a fusion protein of the invention between the Flt1
CC   receptor and the Fc region of IgG. The specification relates to modified
CC   chimeric polypeptides with improved pharmacokinetics. The modified
CC   chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC   been modified to improve their pharmacokinetic profile. The polypeptides
CC   can be used to decrease or inhibit plasma leakage and/or vascular
CC   permeability in a mammal
XX
SQ   Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;
```

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  Query Match             71.7%;  Score 987.4;  DB 5;  Length 1674;
  Best Local Similarity   86.1%;  Pred. No. 1.9e-229;
  Matches 1119;  Conservative    0;  Mismatches  171;  Indels    9;  Gaps    2;

Qy         79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138

Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198

Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258

Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318

Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378
```

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Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438
              ||||||||||      | ||  |  | |   | |  || ||  |   ||  | |  |||
Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498
              ||| | |||||||| || |  |||     | ||   | |  || |  | | ||||   |||
Db        745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy        499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558
              |||  |   |   | ||    ||    | ||  |||  |  |   |      |   ||
Db        805 CCTGATGAAATTGACCAAAGCAATTCCCATGCCAACATATTCTACAGTGTTCTTACTATT 864

Qy        559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618
                | ||| ||||       |      |    ||    | ||||||   ||||||  | |
Db        865 GACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAA---GGAGTGGACCA 921

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678
                |||  |  |   |  | ||          ||  |   |  | ||          | |
Db        922 TCATTCAAATCTGTTAACACCTC------AGTGCATATATATGATAAAGCAGGCCCGGGC 975

Qy        679 AGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 738
                |  | |       ||||||||||||||||||||||||||||||||||||||||||||
Db        976 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 1035

Qy        739 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 1095

Qy        799 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 1155

Qy        859 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 1215

Qy        919 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1275

Qy        979 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1335

Qy       1039 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1395

Qy       1099 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1455

Qy       1159 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1515

Qy       1219 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1516 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1575

Qy       1279 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1635

Qy       1339 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              |||||||||||||||||||||||||||||||||||||||
Db       1636 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1674
```

RESULT 12
ABQ74604

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ID   ABQ74604 standard; cDNA; 1674 BP.
XX
AC   ABQ74604;
XX
DT   23-OCT-2002  (first entry)
XX
DE   Mutation 1 Flt1(1-3 delta B)-Fc nucleotide sequence.
XX
KW   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW   psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW   vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW   ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW   brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW   kidney disease; eye disorder; age-related macular degeneration;
KW   diabetic retinopathy; gene; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1674
FT                   /*tag=  a
FT                   /product= "Mut1:Flt1(1-3 delta B)-Fc protein"
XX
PN   WO200260489-A1.
XX
PD   08-AUG-2002.
XX
PF   28-JAN-2002; 2002WO-US002466.
XX
PR   31-JAN-2001; 2001US-00773877.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Xia Y,  Rudge JS,  Yancopoulos GD;
XX
DR   WPI; 2002-608488/65.
DR   P-PSDB; ABP52443.
XX
PT   Treating psoriasis and enhancing wound healing in humans comprises the
PT   administration of a vascular endothelial cell growth factor (VEGF)
PT   antagonist.
XX
PS   Example 11; Fig 13A-D; 179pp; English.
XX
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence encodes Mut1:Flt1(1-3
CC   delta B)-Fc which is used in an example from the present invention
XX
SQ   Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;

  Query Match            71.7%;  Score 987.4;  DB 6;  Length 1674;
  Best Local Similarity  86.1%;  Pred. No. 1.9e-229;
  Matches 1119;  Conservative    0;  Mismatches  171;  Indels    9;  Gaps    2;

Qy         79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
```

```
Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258

Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318

Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378

Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438

Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498

Db        745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy        499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558

Db        805 CCTGATGAAATTGACCAAAGCAATTCCCATGCCAACATATTCTACAGTGTTCTTACTATT 864

Qy        559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618

Db        865 GACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAA---GGAGTGGACCA 921

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678

Db        922 TCATTCAAATCTGTTAACACCTC------AGTGCATATATATGATAAAGCAGGCCCGGGC 975

Qy        679 AGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 738

Db        976 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 1035

Qy        739 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 798

Db       1036 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 1095

Qy        799 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 858

Db       1096 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 1155

Qy        859 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 918

Db       1156 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 1215

Qy        919 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 978

Db       1216 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1275

Qy        979 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1038

Db       1276 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1335

Qy       1039 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1098

Db       1336 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1395

Qy       1099 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1158

Db       1396 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1455

Qy       1159 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1218

Db       1456 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1515

Qy       1219 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1278

Db       1516 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1575

Qy       1279 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1338

Db       1576 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1635

Qy       1339 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377

Db       1636 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1674
```

RESULT 13
AAA91073
ID AAA91073 standard; DNA; 1704 BP.
XX
AC AAA91073;
XX
DT 05-APR-2001 (first entry)
XX
DE Flt1 receptor fusion protein Mut4:Flt1(1-3R-N)-Fc coding sequence.
XX
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS Unidentified.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1704
FT   /*tag= a
FT   /product= "Flt1(1-3R-N)-Fc"
XX
PN WO200075319-A1.
XX
PD 14-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US014142.
XX
PR 08-JUN-1999; 99US-0138133P.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Papadopoulos NJ, Davis S, Yancopoulos GD;
XX
DR WPI; 2001-071076/08.
DR P-PSDB; AAY97593.
XX
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model
PT systems.
XX
PS Claim 9; Fig 16; 159pp; English.
XX
CC This sequence encodes a fusion protein of the invention between the Flt1
CC receptor and the Fc region of IgG. The specification relates to modified
CC chimeric polypeptides with improved pharmacokinetics. The modified
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC been modified to improve their pharmacokinetic profile. The polypeptides
CC can be used to decrease or inhibit plasma leakage and/or vascular
CC permeability in a mammal
XX
SQ Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;

```
  Query Match             71.3%;  Score 982.4;  DB 5;  Length 1704;
  Best Local Similarity   85.4%;  Pred. No. 3.2e-228;
  Matches 1132;  Conservative    0;  Mismatches  161;  Indels   33;  Gaps    2;

Qy         79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138

Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
```

```
Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438
              ||||||||||     | ||  |  | |    | |  || ||  |   ||  | |  |||
Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498
              ||| | ||||||| || |  |||    | ||   | |  || |  | | ||||   |||
Db        745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy        499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558
              |||  |   ||  || || |         |       |||       ||| | | ||
Db        805 CCTGATGAAAAAAATAAGAACGCTTCCGTAAGGCGACGAATTGACCAAAGCAATTC---- 860

Qy        559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618
              |    || | ||| |  ||     | ||||| ||     |       |  ||| ||
Db        861 --CCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAA 918

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678
              ||| | || || |||   | |   ||||| |       |||       | ||| |  ||
Db        919 GGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAATCTGTTAACACCTCAGTG 978

Qy        679 AGGGTCCATGAAAA----------------------------GGACAAAACTCACACATGC 711
              |  |||| ||                               ||||||||||||||||||
Db        979 CATATATATGATAAAGCAGGCCCGGGCGAGCCCAAATCTTGTGACAAAACTCACACATGC 1038

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 1098

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 1158

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 1218

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1278

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1338

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1398

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1458

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1518

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1578

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1638

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1698

Qy       1372 AAATGA 1377
              ||||||
Db       1699 AAATGA 1704
```

RESULT 14
ABQ74607
ID ABQ74607 standard; cDNA; 1704 BP.
XX
AC ABQ74607;
XX
DT 23-OCT-2002 (first entry)
XX
DE Mutation 4 Flt1(2-3 R->N)-Fc nucleotide sequence.
XX
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW kidney disease; eye disorder; age-related macular degeneration;
KW diabetic retinopathy; gene; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1704
FT   /*tag= a
FT   /product= "Mut4:Flt1(2-3 R->N)-Fc protein"
XX
PN WO200260489-A1.
XX
PD 08-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002466.
XX
PR 31-JAN-2001; 2001US-00773877.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Xia Y, Rudge JS, Yancopoulos GD;
XX
DR WPI; 2002-608488/65.
DR P-PSDB; ABP52446.
XX
PT Treating psoriasis and enhancing wound healing in humans comprises the
PT administration of a vascular endothelial cell growth factor (VEGF)
PT antagonist.
XX
PS Example 14; Fig 16A-D; 179pp; English.
XX
CC The present invention describes a method for treating psoriasis and
CC enhancing wound healing in a mammal or a human. The method comprises
CC administering a vascular endothelial cell growth factor (VEGF) antagonist
CC to the mammal or human. A VEGF antagonist has antipsoriatic,
CC antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC nephrotropic and ophthalmological activities. The method can be used in
CC treating psoriasis and enhancing wound healing in humans by administering
CC VEGF antagonist. The method is also useful in treating clinical
CC conditions characterised by vascular permeability, oedema or
CC inflammation, such as brain oedema associated with injury, oedema
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC asthma, burns, kidney diseases, or eye disorders such as age-related

```
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence encodes Mut4:Flt1(2-3 R-
CC   >N)-Fc which is used in an example from the present invention
XX
SQ   Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;

  Query Match            71.3%;  Score 982.4;  DB 6;  Length 1704;
  Best Local Similarity  85.4%;  Pred. No. 3.2e-228;
  Matches 1132;  Conservative    0;  Mismatches  161;  Indels   33;  Gaps    2;

Qy         79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438
              ||||||||||     | ||  |  | |    | |  || ||  |   ||  | |  |||
Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498
              ||| | ||||||| || |  |||    | ||   | |  || |  | | ||||   |||
Db        745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy        499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558
              |||  |   ||  || || |       |       |||       ||| | | ||
Db        805 CCTGATGAAAAAAATAAGAACGCTTCCGTAAGGCGACGAATTGACCAAAGCAATTC---- 860

Qy        559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618
                 |   || | ||| |  ||     | ||||| ||     |       |  ||| ||
Db        861 --CCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAA 918

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678
              ||| | || || |||    | |   ||||| |       |||       | ||| |  ||
Db        919 GGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAATCTGTTAACACCTCAGTG 978

Qy        679 AGGGTCCATGAAAA----------------------------GGACAAAACTCACACATGC 711
                |  |||| ||                            ||||||||||||||||||
Db        979 CATATATATGATAAAGCAGGCCCGGGCGAGCCCAAATCTTGTGACAAAACTCACACATGC 1038

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 1098

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 1158

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 1218

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1278

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1338

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1398

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1458

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1518

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1578

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1638

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1698

Qy       1372 AAATGA 1377
              ||||||
Db       1699 AAATGA 1704


RESULT 15
AAA91077
ID   AAA91077 standard; DNA; 1704 BP.
XX
AC   AAA91077;
XX
DT   05-APR-2001  (first entry)
XX
DE   Flt1 receptor protein Flt1(1-3)-Fc coding sequence.
XX
KW   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW   plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1704
FT                   /*tag=  a
FT                   /product= "Flt1(1-3)-Fc"
XX
PN   WO200075319-A1.
XX
PD   14-DEC-2000.
XX
PF   23-MAY-2000; 2000WO-US014142.
XX
PR   08-JUN-1999;   99US-0138133P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Papadopoulos NJ,  Davis S,  Yancopoulos GD;
XX
DR   WPI; 2001-071076/08.
DR   P-PSDB; AAY97597.
XX
PT   Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT   and its fragments, useful for diagnosis, evaluation, and treatment of
PT   diseases associated with the gene expression and for producing model
PT   systems.
XX
PS   Example 11; Fig 10; 159pp; English.
XX
```

CC This sequence encodes a fusion protein of the invention between the Flt1
CC receptor and the Fc region of IgG. The specification relates to modified
CC chimeric polypeptides with improved pharmacokinetics. The modified
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC been modified to improve their pharmacokinetic profile. The polypeptides
CC can be used to decrease or inhibit plasma leakage and/or vascular
CC permeability in a mammal
XX
SQ Sequence 1704 BP; 508 A; 460 C; 386 G; 350 T; 0 U; 0 Other;

Query Match 71.2%; Score 980.8; DB 5; Length 1704;
Best Local Similarity 85.3%; Pred. No. 7.8e-228;
Matches 1131; Conservative 0; Mismatches 162; Indels 33; Gaps 2;

```
Qy        79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy       139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy       199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy       259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy       319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy       379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438
             ||||||||||      | ||  | | |     | |  || ||  |   ||  | |  |||
Db       685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy       439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498
             ||| | ||||||| || |  |||    | ||   | |  || |  | | ||||   |||
Db       745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy       499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558
             |||       |  |  |  |||||| |  |      |    | ||    |||
Db       805 CCT------GATGAAAAAAATAAGAGAGCTTCCGTAAGGCGACGAATTGACCAAAGCAAT 858

Qy       559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618
                 |    || | ||| |  ||     | ||||| ||     |       |  ||| ||
Db       859 TCCCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAA 918

Qy       619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678
             ||| | || || |||   | |   ||||| |       |||      | ||| |  ||
Db       919 GGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAATCTGTTAACACCTCAGTG 978

Qy       679 AGGGTCCATGAAAA----------------------------GGACAAAACTCACACATGC 711
                |  |||| ||                            ||||||||||||||||||
Db       979 CATATATATGATAAAGCAGGCCCGGGCGAGCCCAAATCTTGTGACAAAACTCACACATGC 1038

Qy       712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1039 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 1098

Qy       772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1099 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 1158

Qy       832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1159 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 1218

Qy       892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1219 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1278

Qy       952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1279 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1338

Qy      1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1339 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1398

Qy      1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1399 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1458

Qy      1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1459 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1518

Qy      1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1519 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1578

Qy      1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1638

Qy      1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1639 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1698

Qy      1372 AAATGA 1377
             ||||||
Db      1699 AAATGA 1704
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Search completed: September 23, 2005, 14:00:38
Job time : 771 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 13:12:56 ; Search time 4299 Seconds
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Title: US-10-811-170-1
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	684	49.7	871	4	BG753979	602709506
2	684	49.7	983	5	BQ708975	BQ708975 AGENCOURT
3	683	49.6	941	5	BQ712021	BQ712021 AGENCOURT
4	682.4	49.6	843	4	BM007897	603617582
5	682.4	49.6	925	5	BQ709152	BQ709152 AGENCOURT
6	682.4	49.6	1022	3	CR611254	CR611254 full-leng
7	682.4	49.6	1048	3	CR595172	CR595172 full-leng
8	682.4	49.6	1090	3	CR612308	CR612308 full-leng
9	682.4	49.6	1091	3	CR604961	CR604961 full-leng
10	682.4	49.6	1093	3	CR616804	CR616804 full-leng
11	682.4	49.6	1098	3	CR626477	CR626477 full-leng
12	682.4	49.6	1100	3	CR612813	CR612813 full-leng
13	682.4	49.6	1102	3	CR601777	CR601777 full-leng
14	682.4	49.6	1102	3	CR625051	CR625051 full-leng
15	682.4	49.6	1103	3	CR595194	CR595194 full-leng
16	682.4	49.6	1104	3	CR591904	CR591904 full-leng
17	682.4	49.6	1106	3	CR613460	CR613460 full-leng
18	682.4	49.6	1106	3	CR620071	CR620071 full-leng
19	682.4	49.6	1107	3	CR598548	CR598548 full-leng
20	682.4	49.6	1109	3	CR614200	CR614200 full-leng
21	682.4	49.6	1109	3	CR619687	CR619687 full-leng
22	682.4	49.6	1111	3	CR606782	CR606782 full-leng
23	682.4	49.6	1114	3	CR593349	CR593349 full-leng
24	682.4	49.6	1114	3	CR618075	CR618075 full-leng
25	682.4	49.6	1118	3	CR613511	CR613511 full-leng
26	682.4	49.6	1120	3	CR619868	CR619868 full-leng
27	682.4	49.6	1124	3	CR611468	CR611468 full-leng
28	682.4	49.6	1136	3	CR598462	CR598462 full-leng
29	682.4	49.6	1142	3	CR598316	CR598316 full-leng
30	682.4	49.6	1179	3	CR607277	CR607277 full-leng
31	682.4	49.6	1287	3	CR611016	CR611016 full-leng
32	682.4	49.6	1289	3	CR594000	CR594000 full-leng
33	681.4	49.5	851	5	BX346946	BX346946 BX346946
34	681.4	49.5	973	5	BQ706204	BQ706204 AGENCOURT
35	680.8	49.4	919	5	BQ709339	BQ709339 AGENCOURT
36	679.2	49.3	947	5	BQ709771	BQ709771 AGENCOURT
c 37	677	49.2	1013	5	BX360518	BX360518 BX360518
38	676.8	49.2	897	5	BQ709144	BQ709144 AGENCOURT
39	676.6	49.1	757	4	BG674795	BG674795 602620925
40	676.6	49.1	914	5	BQ712363	BQ712363 AGENCOURT
41	676	49.1	881	5	BQ711291	BQ711291 AGENCOURT
42	672	48.8	892	4	BG397723	BG397723 602438784
43	672	48.8	897	4	BM008412	BM008412 603617406
c 44	671.8	48.8	1015	5	BX367600	BX367600 BX367600
45	671.4	48.8	856	5	BQ709859	BQ709859 AGENCOURT

ALIGNMENTS

RESULT 1
BG753979
LOCUS BG753979 871 bp mRNA linear EST 15-MAY-2001
DEFINITION 602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5', mRNA sequence.
ACCESSION BG753979
VERSION BG753979.1 GI:14064632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1686 row: k column: 02
High quality sequence stop: 848.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4846201"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

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  Query Match             49.7%;  Score 684;  DB 4;  Length 871;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-179;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db         37 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 96

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Db         97 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 156

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        157 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 216

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        217 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 276

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        277 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 336

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        337 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 396

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Db        397 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 456

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db        457 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 516

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        517 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 576

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        577 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 636

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        637 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 696

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        697 CTCTCCCTGTCTCCGGGTAAATGA 720


RESULT 2
BQ708975
LOCUS       BQ708975                983 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
            5', mRNA sequence.
ACCESSION   BQ708975
VERSION     BQ708975.1  GI:21847874
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: k  column: 12
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6279683"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             49.7%;  Score 684;  DB 5;  Length 983;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-179;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db         24 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 83

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Db         84 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 143

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        144 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 203

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 263

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 323

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 383

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Db        384 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 443

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db        444 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 503

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        504 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 563

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        624 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 683
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Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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RESULT 3
BQ712021
LOCUS       BQ712021                941 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403
            5', mRNA sequence.
ACCESSION   BQ712021
VERSION     BQ712021.1  GI:21850920
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 941)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2474  row: c  column: 04
            High quality sequence stop: 638.
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                     /clone="IMAGE:6281403"
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                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             49.6%;  Score 683;  DB 5;  Length 941;
  Best Local Similarity   99.9%;  Pred. No. 9.2e-179;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db         50 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 109

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Db        110 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 169

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        170 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 229

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        230 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 289

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        290 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 349

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        350 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 409

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Db        410 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 469

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db        470 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 529

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        530 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 589

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        590 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 649

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        650 AACGTCTTCTCATGCTCCGTGATGCATGANGCTCTGCACAACCACTACACGCAGAAGAGC 709

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        710 CTCTCCCTGTCTCCGGGTAAATGA 733


RESULT 4
BM007897
LOCUS       BM007897                843 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
            mRNA sequence.
ACCESSION   BM007897
VERSION     BM007897.1  GI:16522238
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 843)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1939  row: d  column: 22
            High quality sequence stop: 833.
FEATURES             Location/Qualifiers
     source          1. .843
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5450469"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
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ORIGIN

  Query Match           49.6%;  Score 682.4;  DB 4;  Length 843;
  Best Local Similarity  99.9%;  Pred. No. 1.3e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 167

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 227

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        228 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 287

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        288 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 347

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 407

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        408 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 467

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 527

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 587

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        588 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 647

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        648 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 707

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        708 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCATTACACGCAGAAGAGC 767

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        768 CTCTCCCTGTCTCCGGGTAAATGA 791


RESULT 5
BQ709152
LOCUS       BQ709152                925 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245
            5', mRNA sequence.
ACCESSION   BQ709152
VERSION     BQ709152.1  GI:21848051
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 925)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2516  row: m  column: 22
            High quality sequence stop: 739.
FEATURES             Location/Qualifiers
     source          1. .925
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301245"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match           49.6%;  Score 682.4;  DB 5;  Length 925;
  Best Local Similarity  99.9%;  Pred. No. 1.3e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 107

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 167

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 227

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        228 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 287

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 347

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        348 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 407

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 467

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 527

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        588 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 647

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        648 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 707

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        708 CTCTCCCTGTCTCCGGGTAAATGA 731


RESULT 6
CR611254
LOCUS       CR611254               1022 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DE007YJ17 of Placenta of Homo sapiens
            (human).
ACCESSION   CR611254
VERSION     CR611254.1  GI:50492061
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1022)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1022)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1022
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE007YJ17"
                     /tissue_type="Placenta"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match            49.6%;  Score 682.4;  DB 3;  Length 1022;
  Best Local Similarity  99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        983 CTCTCCCTGTCTCCGGGTAAATGA 1006


RESULT 7
CR595172
LOCUS       CR595172               1048 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI040YA16 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR595172
VERSION     CR595172.1  GI:50475979
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1048)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1048)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1048
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI040YA16"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match            49.6%;  Score 682.4;  DB 3;  Length 1048;
  Best Local Similarity  99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        336 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 395

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 455

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 515

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 575

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 635

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Qy       1054 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        816 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 875

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        936 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 995

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
              |||||||||||||||||||||||||
Db        996 CTCTCCCTGTCTCCGGGTAAATGA 1019


RESULT 8
CR612308
LOCUS       CR612308               1090 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI071YG21 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR612308
VERSION     CR612308.1  GI:50493115
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1090)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1090)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1090
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI071YG21"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             49.6%;  Score 682.4;  DB 3;  Length 1090;
  Best Local Similarity   99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
              |||||||||||||||||||||||||
Db        983 CTCTCCCTGTCTCCGGGTAAATGA 1006


RESULT 9
CR604961
LOCUS       CR604961               1091 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI009YJ10 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR604961
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VERSION     CR604961.1  GI:50485768
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1091)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1091)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1091
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI009YJ10"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match            49.6%;  Score 682.4;  DB 3;  Length 1091;
  Best Local Similarity  99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
              |||||||||||||||||||||||
Db        983 CTCTCCCTGTCTCCGGGTAAATGA 1006


RESULT 10
CR616804
LOCUS       CR616804               1093 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI048YC07 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR616804
VERSION     CR616804.1  GI:50497611
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1093)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1093)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1093
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI048YC07"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match            49.6%;  Score 682.4;  DB 3;  Length 1093;
  Best Local Similarity  99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562
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Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        983 CTCTCCCTGTCTCCGGGTAAATGA 1006
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RESULT 11
CR626477
LOCUS       CR626477               1098 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0CAP001YI13 of Thymus of Homo sapiens
            (human).
ACCESSION   CR626477
VERSION     CR626477.1  GI:50507284
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1098)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1098)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1098
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0CAP001YI13"
                     /tissue_type="Thymus"
                     /plasmid="pCMVSPORT_6"
ORIGIN
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  Query Match            49.6%;  Score 682.4;  DB 3;  Length 1098;
  Best Local Similarity  99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        983 CTCTCCCTGTCTCCGGGTAAATGA 1006
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RESULT 12
CR612813
LOCUS       CR612813               1100 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI081YF02 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR612813
VERSION     CR612813.1  GI:50493620
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1100)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
```

```
REFERENCE   2  (bases 1 to 1100)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1100
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI081YF02"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             49.6%;  Score 682.4;  DB 3;  Length 1100;
  Best Local Similarity   99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 378

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Db        379 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 438

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 498

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 558

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 618

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 678

Qy       1054 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Db        679 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 738

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db        739 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 798

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        799 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 858

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        859 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 918

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        919 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 978

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        979 CTCTCCCTGTCTCCGGGTAAATGA 1002
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RESULT 13
CR601777
LOCUS       CR601777               1102 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0CAP008YF07 of Thymus of Homo sapiens
            (human).
ACCESSION   CR601777
VERSION     CR601777.1  GI:50482584
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1102)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1102)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1102
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             49.6%;  Score 682.4;  DB 3;  Length 1102;
  Best Local Similarity   99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db        319 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 378

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Db        379 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 438

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        439 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 498

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        499 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 558

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        559 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 618

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        619 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 678

Qy       1054 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Db        679 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 738
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Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db        739 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 798

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        799 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 858

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        859 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 918

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        919 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 978

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        979 CTCTCCCTGTCTCCGGGTAAATGA 1002


RESULT 14
CR625051
LOCUS       CR625051               1102 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI059YL06 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR625051
VERSION     CR625051.1  GI:50505858
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1102)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1102)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1102
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                     /db_xref="taxon:9606"
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                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             49.6%;  Score 682.4;  DB 3;  Length 1102;
  Best Local Similarity   99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy       1054 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

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Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

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Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        983 CTCTCCCTGTCTCCGGGTAAATGA 1006


RESULT 15
CR595194
LOCUS       CR595194               1103 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DE010YH13 of Placenta of Homo sapiens
            (human).
ACCESSION   CR595194
VERSION     CR595194.1  GI:50476001
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1103)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1103)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           49.6%;  Score 682.4;  DB 3;  Length 1103;
  Best Local Similarity 99.9%;  Pred. No. 1.4e-178;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db        319 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 378

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 438

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        439 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 498

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        499 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 558

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db        619 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 678

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Db        739 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 798

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Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        919 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 978

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Job time : 4305 secs
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GenCore version 5.1.6

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1377	100.0	1377	4	US-09-773-877B-25	Sequence 25, Appl
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3	1049.2	76.2	1444	4	US-09-773-877B-23	Sequence 23, Appl
4	1039	75.5	1359	4	US-09-773-877B-15	Sequence 15, Appl
5	1032.4	75.0	1389	4	US-09-773-877B-17	Sequence 17, Appl
6	987.4	71.7	1674	4	US-09-773-877B-13	Sequence 13, Appl
7	982.4	71.3	1704	4	US-09-773-877B-19	Sequence 19, Appl
8	980.8	71.2	1704	4	US-09-773-877B-11	Sequence 11, Appl
9	686	49.8	2043	3	US-08-227-496C-14	Sequence 14, Appl
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12	684	49.7	1019	4	US-09-761-413-1	Sequence 1, Appli
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44	684	49.7	9209	1	US-08-476-275-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 25, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VEGFR1R2.FcdeltaC1(a) Receptor
; NAME/KEY: CDS
; LOCATION: (1)..(1377)
US-09-773-877B-25

Query Match 100.0%; Score 1377; DB 4; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
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Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377


RESULT 2
US-09-773-877B-21
; Sequence 21, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
;   LENGTH: 1453
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1D2.Flk1D3.FcdeltaC1(a)Receptor
;   NAME/KEY: CDS
;   LOCATION: (69)..(1442)
US-09-773-877B-21

  Query Match             96.5%;  Score 1328.4;  DB 4;  Length 1453;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1367;  Conservative    0;  Mismatches    1;  Indels   18;  Gaps    2;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||          ||||||||||||||||||||||||||||||||||
Db        129 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 179

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 239

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 299

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 359

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 539

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 599

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 659

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAG---------GACAAAACTCACACATGC 711
              ||||||||||||||||||||||||||||||||          ||||||||||||||||||
Db        720 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGGCCCGGGCGACAAAACTCACACATGC 779

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 839
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Qy       772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
Db       840 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 899

Qy       832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
Db       900 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 959

Qy       892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
Db       960 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1019

Qy       952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
Db      1020 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1079

Qy      1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
Db      1080 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1139

Qy      1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
Db      1140 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1199

Qy      1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
Db      1200 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1259

Qy      1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
Db      1260 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1319

Qy      1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
Db      1320 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1379

Qy      1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
Db      1380 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1439

Qy      1372 AAATGA 1377
Db      1440 AAATGA 1445
```

RESULT 3
US-09-773-877B-23
; Sequence 23, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1D2.VEGFR3D3.FcdeltaC1(a)Receptor
; NAME/KEY: CDS
; LOCATION: (69)..(1436)
US-09-773-877B-23

Query Match 76.2%; Score 1049.2; DB 4; Length 1444;
Best Local Similarity 86.7%; Pred. No. 6.7e-271;
Matches 1201; Conservative 0; Mismatches 158; Indels 27; Gaps 3;

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Qy         1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
Db        69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy        61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
Db       129 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 179

Qy       121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
Db       180 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 239

Qy       181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
Db       240 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 299

Qy       241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
Db       300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 359

Qy       301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
Db       360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy       361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
Db       420 CATCGACAAACCAATACAATCATAGATATCCAGCTGTTGCCCAGGAAGTCGCTGGAGCTG 479

Qy       421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
Db       480 CTGGTAGGGGAGAAGCTGGTCCTCAACTGCACCGTGTGGGCTGAGTTTAACTCAGGTGTC 539

Qy       481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
Db       540 ACCTTTGACTGGGACTACCCAGGGAAGCAGGCAGAGCGGGGTAAGTGGGTGCCCGAGCGA 599

Qy       541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
Db       600 CGCTCCCAACAGACCCACACAG---------AACTCTCCAGCATCCTGACCATCCACAAC 650

Qy       601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
Db       651 GTCAGCCAGCACGACCTGGGCTCGTATGTGTGCAAGGCCAACAACGGCATCCAGCGATTT 710

Qy       661 AAGAACAGCACATTTGTCAGGGTCCATGAAAA---------GGACAAAACTCACACATGC 711
Db       711 CGGGAGAGCACCGAGGTCATTGTGCATGAAAATGGCCCGGGCGACAAAACTCACACATGC 770

Qy       712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
Db       771 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 830

Qy       772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
Db       831 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 890

Qy       832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
Db       891 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 950

Qy       892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
Db       951 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1010

Qy       952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
Db      1011 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1070

Qy      1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
Db      1071 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1130

Qy      1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
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Db       1131 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1190

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1250

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1310

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1370

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1430

Qy       1372 AAATGA 1377
             ||||||
Db       1431 AAATGA 1436


RESULT 4
US-09-773-877B-15
; Sequence 15, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
;   LENGTH: 1359
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1(2-3 deltaB)-Fc(Mut2)
;   NAME/KEY: CDS
;   LOCATION: (1)..(1359)
US-09-773-877B-15

  Query Match             75.5%;  Score 1039;  DB 4;  Length 1359;
  Best Local Similarity   86.3%;  Pred. No. 3.5e-268;
  Matches 1189;  Conservative    0;  Mismatches  170;  Indels   18;  Gaps    3;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||         ||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 111

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 171

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 231

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 291

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 351

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||     || ||  | | |    | |  || ||
Db        352 CATCGACAAACCAATACAATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTA 411

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
                |  ||  | |  |||||| | |||||||| || |  |||    | ||   | |  ||
Db        412 CTTAGAGGCCATACTCTTGTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTT 471

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              |  | | ||||   ||||||  |    |  | ||    ||    | ||  |||  |  |
Db        472 CAAATGACCTGGAGTTACCCTGATGAAATTGACCAAAGCAATTCCCATGCCAACATATTC 531

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
                |    |   ||       | ||| ||||          |     |    ||    | ||
Db        532 TACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGT 591

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||   ||||||  | |  |||  |  |   |   | ||       ||   |   |
Db        592 GTAA---GGAGTGGACCATCATTCAAATCTGTTAACACCTC------AGTGCATATATAT 642

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              | ||          | |  |  | |        ||||||||||||||||||||||||||
Db        643 GATAAAGCAGGCCCGGGCGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 702

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 762

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 822

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        823 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 882

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 942

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1002

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1062

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1122

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1182

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1242

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1302

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1359


RESULT 5
US-09-773-877B-17
; Sequence 17, Application US/09773877B
; Patent No. 6833349
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; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 1389
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1(2-3)-Fc (Mut3)
;   NAME/KEY: CDS
;   LOCATION: (1)..(1389)
US-09-773-877B-17

  Query Match             75.0%;  Score 1032.4;  DB 4;  Length 1389;
  Best Local Similarity   85.5%;  Pred. No. 2.1e-266;
  Matches 1201;  Conservative    0;  Mismatches  161;  Indels   42;  Gaps    3;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||         ||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 111

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 171

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 231

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 291

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 351

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||     | ||  |  | |    | |  || ||
Db        352 CATCGACAAACCAATACAATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTA 411

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              |   ||  | |  |||||| | |||||||| || |  |||    | ||   | |  ||
Db        412 CTTAGAGGCCATACTCTTGTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTT 471

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              |  | | ||||   ||||||       |  |  |  |||||| |  |       |
Db        472 CAAATGACCTGGAGTTACCCT------GATGAAAAAAATAAGAGAGCTTCCGTAAGGCGA 525

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              | ||    |||           |    || | ||| |  ||     | ||||| ||
Db        526 CGAATTGACCAAAGCAATTCCCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAA 585

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              |       |  ||| ||||| | || || |||   | |   ||||| |       |||
Db        586 ATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAA 645

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAA----------------------------G 693
              | ||| |  ||     |  |||| ||
Db        646 TCTGTTAACACCTCAGTGCATATATATGATAAAGCAGGCCCGGGCGAGCCCAAATCTTGT 705

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 765

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 825

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 885

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 945

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 1005

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1065

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1125

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1185

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1245

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1305

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1365

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
              |||||||||||||||||||||||||
Db       1366 CTCTCCCTGTCTCCGGGTAAATGA 1389


RESULT 6
US-09-773-877B-13
; Sequence 13, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS:. 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 1674
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1(1-3 deltaB)(Mut 1)
;   NAME/KEY: CDS
;   LOCATION: (1)..(1674)
US-09-773-877B-13

  Query Match             71.7%;  Score 987.4;  DB 4;  Length 1674;
  Best Local Similarity   86.1%;  Pred. No. 2.6e-254;
  Matches 1119;  Conservative    0;  Mismatches  171;  Indels    9;  Gaps    2;

Qy         79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138
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Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198

Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258

Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318

Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378

Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438

Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498

Db        745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy        499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558

Db        805 CCTGATGAAATTGACCAAAGCAATTCCCATGCCAACATATTCTACAGTGTTCTTACTATT 864

Qy        559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618

Db        865 GACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAA---GGAGTGGACCA 921

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678

Db        922 TCATTCAAATCTGTTAACACCTC------AGTGCATATATATGATAAAGCAGGCCCGGGC 975

Qy        679 AGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 738

Db        976 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 1035

Qy        739 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 798

Db       1036 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 1095

Qy        799 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 858

Db       1096 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 1155

Qy        859 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 918

Db       1156 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 1215

Qy        919 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 978

Db       1216 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1275

Qy        979 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1038

Db       1276 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1335

Qy       1039 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1098

Db       1336 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1395

Qy       1099 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1158

Db       1396 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1455

Qy       1159 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1218

Db       1456 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1515

Qy       1219 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1278

Db       1516 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1575

Qy       1279 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1338

Db       1576 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1635

Qy       1339 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377

Db       1636 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1674
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RESULT 7
US-09-773-877B-19
; Sequence 19, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1704
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(1-3 R->N)(Mut 4)
; NAME/KEY: CDS
; LOCATION: (1)..(1704)
US-09-773-877B-19

Query Match 71.3%; Score 982.4; DB 4; Length 1704;
Best Local Similarity 85.4%; Pred. No. 5.7e-253;
Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;

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Qy          79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138

Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198

Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258

Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318

Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378

Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438

Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498

Db        745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy        499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558

Db        805 CCTGATGAAAAAAATAAGAACGCTTCCGTAAGGCGACGAATTGACCAAAGCAATTC---- 860
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Qy        559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618
Db        861 --CCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAA 918

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678
Db        919 GGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAATCTGTTAACACCTCAGTG 978

Qy        679 AGGGTCCATGAAAA----------------------------GGACAAAACTCACACATGC 711
Db        979 CATATATATGATAAAGCAGGCCCGGGCGAGCCCAAATCTTGTGACAAAACTCACACATGC 1038

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
Db       1039 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 1098

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
Db       1099 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 1158

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
Db       1159 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 1218

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
Db       1219 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1278

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
Db       1279 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1338

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
Db       1339 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1398

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
Db       1399 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1458

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
Db       1459 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1518

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
Db       1519 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1578

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
Db       1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1638

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
Db       1639 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1698

Qy       1372 AAATGA 1377
Db       1699 AAATGA 1704
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RESULT 8
US-09-773-877B-11
; Sequence 11, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 11
; LENGTH: 1704
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(1-3)-Fc
; NAME/KEY: CDS
; LOCATION: (1)..(1704)
US-09-773-877B-11

Query Match 71.2%; Score 980.8; DB 4; Length 1704;
Best Local Similarity 85.3%; Pred. No. 1.5e-252;
Matches 1131; Conservative 0; Mismatches 162; Indels 33; Gaps 2;

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Qy         79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138
Db        385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 444

Qy        139 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
Db        445 ACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 504

Qy        199 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258
Db        505 TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 564

Qy        259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318
Db        565 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624

Qy        319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378
Db        625 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684

Qy        379 ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 438
Db        685 ATCATAGATGTCCAAATAAGCACACCACGCCCAGTCAAATTACTTAGAGGCCATACTCTT 744

Qy        439 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498
Db        745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804

Qy        499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558
Db        805 CCT------GATGAAAAAAATAAGAGAGCTTCCGTAAGGCGACGAATTGACCAAAGCAAT 858

Qy        559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA 618
Db        859 TCCCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGACAAA 918

Qy        619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC 678
Db        919 GGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAATCTGTTAACACCTCAGTG 978

Qy        679 AGGGTCCATGAAAA----------------------------GGACAAAACTCACACATGC 711
Db        979 CATATATATGATAAAGCAGGCCCGGGCGAGCCCAAATCTTGTGACAAAACTCACACATGC 1038

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
Db       1039 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 1098

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
Db       1099 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 1158

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
Db       1159 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 1218

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
Db       1219 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1278
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Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1338

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1398

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1458

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1518

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1578

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1638

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1698

Qy       1372 AAATGA 1377
              ||||||
Db       1699 AAATGA 1704
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```
RESULT 9
US-08-227-496C-14
; Sequence 14, Application US/08227496C
; Patent No. 6130202
;  GENERAL INFORMATION:
;    APPLICANT:  Greve, Jeffrey M.
;    APPLICANT:  McClelland, Alan
;    TITLE OF INVENTION:  Multimeric Forms of Human
;    TITLE OF INVENTION:  Rhinovirus Receptor Protein
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bayer Corporation
;      STREET:  400 Morgan Lane
;      CITY:  West Haven
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06516
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  diskette, 1.44 Mb storage
;      COMPUTER:  Dell OptiPlex GX1
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/227,496C
;      FILING DATE:  04/14/94
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/903,069
;      FILING DATE:  06/22/92
;      APPLICATION NUMBER:  07/704,984
;      FILING DATE:  05/24/91
;      APPLICATION NUMBER:  07/556,238
;      FILING DATE:  07/20/90
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barbara A. Shimei
;      REGISTRATION NUMBER:  29,862
;      REFERENCE/DOCKET NUMBER:  MTI 214.2C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 812-2786
;      TELEFAX:  (203) 812-5492
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2043 bp
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FEATURE:
;      NAME/KEY:  tICAM(453)/IgG fusion
;      OTHER INFORMATION:  bp 1-1359 = nucleotides coding
;      OTHER INFORMATION:  for amino acid residues 1-453 of ICAM-1; bp 1360-
;      OTHER INFORMATION:  2040 = nucleotides coding for amino acid residues
;      OTHER INFORMATION:  216-442 of human heavy chain IgG1; bp 2401-2043 =
;      OTHER INFORMATION:  stop codon
US-08-227-496C-14

  Query Match             49.8%;  Score 686;  DB 3;  Length 2043;
  Best Local Similarity   95.9%;  Pred. No. 1.6e-173;
  Matches  704;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy        644 GTGGGCTGATGACCAAGAAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTC 703
              | | | | |    |||| || |   |   | ||     ||   | ||||||||||||
Db       1310 GGGAGGTCACCCGCAAGGTGACCGTGAATGTGCTCTCCCCCCGGTATGAGGACAAAACTC 1369

Qy        704 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1370 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 1429

Qy        764 CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1430 CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 1489

Qy        824 TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1490 TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 1549

Qy        884 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA 943
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1550 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCA 1609

Qy        944 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1610 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 1669

Qy       1004 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1670 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1729

Qy       1064 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1730 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 1789

Qy       1124 GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA 1183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1790 GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA 1849

Qy       1184 ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCT 1243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1850 ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCT 1909

Qy       1244 TCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCT 1303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1910 TCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCT 1969

Qy       1304 CATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGT 1363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1970 CATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGT 2029

Qy       1364 CTCCGGGTAAATGA 1377
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Db       2030 CTCCGGGTAAATGA 2043


RESULT 10
US-09-023-655-1223
; Sequence 1223, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1223:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  705 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g243865
US-09-023-655-1223

  Query Match             49.7%;  Score 684;  DB 4;  Length 705;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-173;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 64

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 124

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 184

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 244

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 304

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 364

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 424

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 484

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 544

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 604

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 664

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        665 CTCTCCCTGTCTCCGGGTAAATGA 688


RESULT 11
US-09-178-869-1
; Sequence 1, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
;  APPLICANT: Tao, Weng
;  APPLICANT: Wong, Shou
;  APPLICANT: Hickey, William F
;  APPLICANT: Hammang, Joseph P.
;  APPLICANT: Baetge, E. Edward
;  TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
;  FILE REFERENCE: 17810-043
;  CURRENT APPLICATION NUMBER: US/09/178,869B
;  CURRENT FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: ()..)
;   OTHER INFORMATION: Description of Sequence: Recombinant
;   OTHER INFORMATION: Polynucleotide
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (16)..(1008)
US-09-178-869-1

  Query Match             49.7%;  Score 684;  DB 3;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 4e-173;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 387

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 447
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Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 507

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 567

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 627

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 687

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 747

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 807

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 867

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 927

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 987

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
              |||||||||||||||||||||||||
Db        988 CTCTCCCTGTCTCCGGGTAAATGA 1011
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RESULT 12
US-09-761-413-1
; Sequence 1, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/761,413
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/178,869
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1019
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: ()..)
; OTHER INFORMATION: Description of Sequence: Recombinant
; OTHER INFORMATION: Polynucleotide
; NAME/KEY: CDS
; LOCATION: (16)..(1008)
US-09-761-413-1

Query Match 49.7%; Score 684; DB 4; Length 1019;
Best Local Similarity 100.0%; Pred. No. 4e-173;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 387

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 447

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 507

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 567

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        568 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 627

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 687

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 747

Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db        748 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 807

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db        808 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 867

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        868 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 927

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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RESULT 13
US-09-180-100-18
; Sequence 18, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-180-100-18

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  Query Match           49.7%;  Score 684;  DB 3;  Length 1182;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-173;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        603 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 662

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Db        663 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 722

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        723 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 782

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Qy       1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1173
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Db        903 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 962

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Db         963 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1022

Qy       1234 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
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Db        1023 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1082

Qy       1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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Db        1083 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1142

Qy       1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
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Db        1143 CTCTCCCTGTCTCCGGGTAAATGA 1166


RESULT 14
US-08-488-376-19
; Sequence 19, Application US/08488376
; Patent No. 5811524
;  GENERAL INFORMATION:
;    APPLICANT:  BRAMS, Peter
;    APPLICANT:  CHAMAT, Soulaima Salim
;    APPLICANT:  PAN, Li-Zhen
;    APPLICANT:  WALSH, Edward E.
;    APPLICANT:  HEARD, Cheryl Janne
;    APPLICANT:  NEWMAN, Roland Anthony
;    TITLE OF INVENTION:  NEUTRALIZING HIGH AFFINITY HUMAN
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;    TITLE OF INVENTION:  METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,376
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-150
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1428 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1428
US-08-488-376-19

  Query Match           49.7%;  Score 684;  DB 1;  Length 1428;
  Best Local Similarity  100.0%;  Pred. No. 4.6e-173;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db        745 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 804

Qy        754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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Db        805 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 864

Qy        814 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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Db        865 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 924

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 984

Qy        934 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
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Db        985 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 1044

Qy        994 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
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Db       1045 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1104

Qy       1054 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
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Db       1105 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1164

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Db       1165 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1224

Qy       1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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RESULT 15
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; Sequence 19, Application US/08634223
; Patent No. 5840298
;  GENERAL INFORMATION:
;    APPLICANT:  BRAMS, Peter
;    APPLICANT:  CHAMAT, Soulaima Salim
;    APPLICANT:  PAN, Li-Zhen
;    APPLICANT:  WALSH, Edward E.
;    APPLICANT:  HEARD, Cheryl Janne
;    APPLICANT:  NEWMAN, Roland Anthony
;    TITLE OF INVENTION:  NEUTRALIZING HIGH AFFINITY HUMAN
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;    TITLE OF INVENTION:  METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/634,223
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,376
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-150
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1428 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1428
US-08-634-223-19

  Query Match             49.7%;  Score 684;  DB 2;  Length 1428;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-173;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 753
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Db        745 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 804

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Db        865 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 924

Qy        874 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 933
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Total number of hits satisfying chosen parameters: 14801408

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1377	100.0	1377	10	US-09-773-877A-25	Sequence 25, Appl
2	1377	100.0	1377	17	US-10-609-775-9	Sequence 9, Appli
3	1377	100.0	1377	20	US-10-860-958-1	Sequence 1, Appli
4	1377	100.0	1377	21	US-10-830-902-1	Sequence 1, Appli
5	1377	100.0	1377	21	US-10-897-802-1	Sequence 1, Appli
6	1377	100.0	1377	21	US-10-880-021-9	Sequence 9, Appli
7	1377	100.0	1377	21	US-10-909-011-3	Sequence 3, Appli
8	1377	100.0	1377	22	US-10-988-243-15	Sequence 15, Appl
9	1377	100.0	1377	22	US-10-998-881-3	Sequence 3, Appli
10	1377	100.0	1377	24	US-11-016-097-15	Sequence 15, Appl
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14	1328.4	96.5	1453	21	US-10-880-021-7	Sequence 7, Appli
15	1328.4	96.5	1453	21	US-10-909-011-1	Sequence 1, Appli
16	1328.4	96.5	1453	22	US-10-988-243-11	Sequence 11, Appl
17	1328.4	96.5	1453	22	US-10-998-881-1	Sequence 1, Appli
18	1328.4	96.5	1453	24	US-11-016-097-11	Sequence 11, Appl
19	1323.6	96.1	1377	21	US-10-855-559-12	Sequence 12, Appl
20	1049.2	76.2	1444	10	US-09-773-877A-23	Sequence 23, Appl
21	1049.2	76.2	1444	17	US-10-609-775-12	Sequence 12, Appl
22	1049.2	76.2	1444	21	US-10-880-021-12	Sequence 12, Appl
23	1049.2	76.2	1444	22	US-10-988-243-13	Sequence 13, Appl
24	1049.2	76.2	1444	24	US-11-016-097-13	Sequence 13, Appl
25	1039	75.5	1359	10	US-09-773-877A-15	Sequence 15, Appl
26	1039	75.5	1359	22	US-10-988-243-5	Sequence 5, Appli
27	1039	75.5	1359	24	US-11-016-097-5	Sequence 5, Appli
28	1032.4	75.0	1389	10	US-09-773-877A-17	Sequence 17, Appl
29	1032.4	75.0	1389	22	US-10-988-243-7	Sequence 7, Appli
30	1032.4	75.0	1389	24	US-11-016-097-7	Sequence 7, Appli
31	987.4	71.7	1674	10	US-09-773-877A-13	Sequence 13, Appl
32	987.4	71.7	1674	22	US-10-988-243-3	Sequence 3, Appli
33	987.4	71.7	1674	24	US-11-016-097-3	Sequence 3, Appli
34	982.4	71.3	1704	10	US-09-773-877A-19	Sequence 19, Appl
35	982.4	71.3	1704	22	US-10-988-243-9	Sequence 9, Appli
36	982.4	71.3	1704	24	US-11-016-097-9	Sequence 9, Appli
37	980.8	71.2	1704	10	US-09-773-877A-11	Sequence 11, Appl
38	980.8	71.2	1704	22	US-10-988-243-1	Sequence 1, Appli
39	980.8	71.2	1704	24	US-11-016-097-1	Sequence 1, Appli
40	687.8	49.9	1290	17	US-10-435-608-7	Sequence 7, Appli
41	687.8	49.9	1290	18	US-10-622-108-7	Sequence 7, Appli
42	687.8	49.9	1299	17	US-10-435-608-9	Sequence 9, Appli
43	687.8	49.9	1299	18	US-10-622-108-9	Sequence 9, Appli
44	687.2	49.9	1383	17	US-10-275-589-17	Sequence 17, Appl
45	687.2	49.9	1389	17	US-10-385-802-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-773-877A-25
; Sequence 25, Application US/09773877A
; Publication No. US20030017977A1
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877A
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VEGFR1R2.FcdeltaC1(a) Receptor
; NAME/KEY: CDS
; LOCATION: (1)..(1377)
US-09-773-877A-25

Query Match 100.0%; Score 1377; DB 10; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

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Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
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RESULT 2
US-10-609-775-9
; Sequence 9, Application US/10609775
; Publication No. US20040014667A1
; GENERAL INFORMATION:
; APPLICANT: Thomas J. Daly
; APPLICANT: James P. Fandl
; APPLICANT: Nicholas J. Papadopoulos
; TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: REG 710D
; CURRENT APPLICATION NUMBER: US/10/609,775
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-609-775-9

Query Match 100.0%; Score 1377; DB 17; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
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Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
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Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
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RESULT 3
US-10-860-958-1
; Sequence 1, Application US/10860958
; Publication No. US20040265309A1
; GENERAL INFORMATION:
; APPLICANT: Kandel, Jessica
; APPLICANT: Holash, Jocelyn
; APPLICANT: Yamashiro, Darrell
; APPLICANT: Huang, Jianzhong
; APPLICANT: Yancopoulos, George
; APPLICANT: Rudge, John
; TITLE OF INVENTION: Method of Tumor Regression with VEGF
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: REG 714A
; CURRENT APPLICATION NUMBER: US/10/860,958
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/476,425
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-860-958-1

Query Match 100.0%; Score 1377; DB 20; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
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Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
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Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377


RESULT 4
US-10-830-902-1
; Sequence 1, Application US/10830902
; Publication No. US20050004027A1
; GENERAL INFORMATION:
;  APPLICANT: Stanley Wiegand
;  APPLICANT:  Jingtai Cao
;  APPLICANT:  Claus Cursiefien
;  TITLE OF INVENTION: Method of Treating Corneal Transplant
;  TITLE OF INVENTION:  Rejection
;  FILE REFERENCE: REG 713B
;  CURRENT APPLICATION NUMBER: US/10/830,902
;  CURRENT FILING DATE:  2004-04-23
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-830-902-1

  Query Match             100.0%;  Score 1377;  DB 21;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||.
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377


RESULT 5
US-10-897-802-1
; Sequence 1, Application US/10897802
; Publication No. US20050032699A1
; GENERAL INFORMATION:
;  APPLICANT: Jocelyn Holash
;  APPLICANT:  Robert Jaffe
;  APPLICANT:  Limin Hu
;  APPLICANT:  George D. Yancopoulos
;  TITLE OF INVENTION: Composition of a VEGF Antagonist and an Anti-Proliferative Agent
;  FILE REFERENCE: REG 715B
;  CURRENT APPLICATION NUMBER: US/10/897,802
;  CURRENT FILING DATE:  2004-07-23
;  PRIOR APPLICATION NUMBER: 60/493,971
;  PRIOR FILING DATE: 2003-08-08
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-897-802-1

  Query Match             100.0%;  Score 1377;  DB 21;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
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Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
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Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
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Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377


RESULT 6
US-10-880-021-9
; Sequence 9, Application US/10880021
; Publication No. US20050043236A1
; GENERAL INFORMATION:
;  APPLICANT: Daly, thomas J.
;  APPLICANT:  Fandl, James P.
;  APPLICANT:  Papadopoulos, Nicholas J.
;  TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof
;  FILE REFERENCE: RGE 710D2
;  CURRENT APPLICATION NUMBER: US/10/880,021
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;  CURRENT FILING DATE:  2004-06-29
;  PRIOR APPLICATION NUMBER: 10/609,775
;  PRIOR FILING DATE: 2003-06-30
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-880-021-9

  Query Match             100.0%;  Score 1377;  DB 21;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
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Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377


RESULT 7
US-10-909-011-3
; Sequence 3, Application US/10909011
; Publication No. US20050112061A1
; GENERAL INFORMATION:
;  APPLICANT: Jocelyn Holash
;  APPLICANT:  George Yancopoulos
;  APPLICANT:  Phyllis R. Wachsberger
;  APPLICANT:  Adam P. Dicker
;  APPLICANT:  Randy Burd
;  TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
;  FILE REFERENCE: REG 716A
;  CURRENT APPLICATION NUMBER: US/10/909,011
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: 60/492,864
;  PRIOR FILING DATE: 2003-08-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-909-011-3

  Query Match             100.0%;  Score 1377;  DB 21;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
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RESULT 8
US-10-988-243-15
; Sequence 15, Application US/10988243
; Publication No. US20050175610A1
; GENERAL INFORMATION:
; APPLICANT: Wiegand, Stanley
; APPLICANT: Papadopoulos, Nicholas J.
; APPLICANT: Yancopoulos, George
; TITLE OF INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinectic Pro
; TITLE OF INVENTION: and Methods of Making and Using Thereof
; FILE REFERENCE: REG 710F
; CURRENT APPLICATION NUMBER: US/10/988,243
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-988-243-15

Query Match 100.0%; Score 1377; DB 22; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
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Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
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Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
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Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
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RESULT 9
US-10-998-881-3
; Sequence 3, Application US/10998881
; Publication No. US20050196340A1
; GENERAL INFORMATION:
;  APPLICANT: Jocelyn Holash
;  APPLICANT:  George Yancopoulos
;  APPLICANT:  Phyllis R. Wachsberger
;  APPLICANT:  Adam P. Dicker
;  APPLICANT:  Randy Burd
;  TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
;  FILE REFERENCE: 716B
;  CURRENT APPLICATION NUMBER: US/10/998,881
;  CURRENT FILING DATE:  2004-11-29
;  PRIOR APPLICATION NUMBER: 10/909,011
;  PRIOR FILING DATE: 2004-07-30
;  PRIOR APPLICATION NUMBER: 60/492,864
;  PRIOR FILING DATE: 2003-08-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-998-881-3

  Query Match             100.0%;  Score 1377;  DB 22;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
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Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
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Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
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Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
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RESULT 10
US-11-016-097-15
; Sequence 15, Application US/11016097
; Publication No. US20050163798A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,097
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1374)
US-11-016-097-15

Query Match 100.0%; Score 1377; DB 24; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
```

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Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377


RESULT 11
US-11-039-144-1
; Sequence 1, Application US/11039144
; Publication No. US20050197291A1
; GENERAL INFORMATION:
;  APPLICANT: Stanley Wiegand
;  APPLICANT:  Jingtai Cao
;  APPLICANT:  Claus Cursiefien
;  TITLE OF INVENTION: Method of Treating Corneal Transplant
;  TITLE OF INVENTION:  Rejection In High Risk Keratoplasty Patients
;  FILE REFERENCE: 713C
;  CURRENT APPLICATION NUMBER: US/11/039,144
;  CURRENT FILING DATE:  2005-01-19
;  PRIOR APPLICATION NUMBER: 10/830,902
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: 60/473,734
;  PRIOR FILING DATE: 2003-05-28
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-11-039-144-1

  Query Match             100.0%;  Score 1377;  DB 24;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
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Db        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
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Db        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACATGCCCACCGTGC 720

Qy        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 780

Qy        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 840

Qy        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 900

Qy        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 960

Qy        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020

Qy       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1080

Qy       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1140

Qy       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1200

Qy       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1260

Qy       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320

Qy       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1377


RESULT 12
US-09-773-877A-21
; Sequence 21, Application US/09773877A
; Publication No. US20030017977A1
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
```

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;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877A
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
;   LENGTH: 1453
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1D2.Flk1D3.FcdeltaC1(a)Receptor
;   NAME/KEY: CDS
;   LOCATION: (69)..(1442)
US-09-773-877A-21

  Query Match             96.5%;  Score 1328.4;  DB 10;  Length 1453;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1367;  Conservative    0;  Mismatches    1;  Indels   18;  Gaps    2;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              ||||||||||||||||||          ||||||||||||||||||||||||||||||||||||
Db        129 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 179

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 239

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 299

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 359

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 539

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 599

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 659

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAG---------GACAAAACTCACACATGC 711
              ||||||||||||||||||||||||||||||||          ||||||||||||||||||
Db        720 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGGCCCGGGCGACAAAACTCACACATGC 779

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 839

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 899

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 959

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1019

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1079

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1080 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1139

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
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Db       1140 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1199

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1259

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1319

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1379

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1439

Qy       1372 AAATGA 1377
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Db       1440 AAATGA 1445


RESULT 13
US-10-609-775-7
; Sequence 7, Application US/10609775
; Publication No. US20040014667A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas J. Daly
;  APPLICANT:  James P. Fandl
;  APPLICANT:  Nicholas J. Papadopoulos
;  TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: REG 710D
;  CURRENT APPLICATION NUMBER: US/10/609,775
;  CURRENT FILING DATE:  2003-06-30
;  PRIOR APPLICATION NUMBER: 10/009,852
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: PCT/US00/14142
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/138,133
;  PRIOR FILING DATE: 1999-06-08
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1453
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-609-775-7

  Query Match             96.5%;  Score 1328.4;  DB 17;  Length 1453;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1367;  Conservative    0;  Mismatches    1;  Indels   18;  Gaps    2;
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Db         69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
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Db        129 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 179

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
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Db        180 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 239

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
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Db        240 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 299

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 359

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
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Db        360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 539

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
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Db        540 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 599

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 659

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
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Db        660 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAG---------GACAAAACTCACACATGC 711
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Db        720 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGGCCCGGGCGACAAAACTCACACATGC 779

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
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Db        780 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 839

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 899

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
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Db        900 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 959

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1019

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
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Db       1020 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1079

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
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Db       1080 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1139

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1199

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
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Db       1200 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1259

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
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Db       1260 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1319

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
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Db       1320 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1379

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
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Qy       1372 AAATGA 1377
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RESULT 14
US-10-880-021-7
; Sequence 7, Application US/10880021
; Publication No. US20050043236A1
; GENERAL INFORMATION:
; APPLICANT: Daly, thomas J.
; APPLICANT: Fandl, James P.
; APPLICANT: Papadopoulos, Nicholas J.
; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof
; FILE REFERENCE: RGE 710D2
; CURRENT APPLICATION NUMBER: US/10/880,021
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/609,775
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1453
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-880-021-7

Query Match 96.5%; Score 1328.4; DB 21; Length 1453;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;

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Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
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Db         69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
              |||||||||||||||||          ||||||||||||||||||||||||||||||||||
Db        129 ACAGGATCTAGTTCCGGA---------GGTAGACCTTTCGTAGAGATGTACAGTGAAATC 179

Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 239

Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 299

Qy        241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
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Db        300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 359

Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
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Db        360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419

Qy        361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
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Db        420 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
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Db        480 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 539

Qy        481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 599

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Db        600 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 659

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Db        660 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719

Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAG---------GACAAAACTCACACATGC 711
              |||||||||||||||||||||||||||||||         |||||||||||||||||||
Db        720 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGGCCCGGGCGACAAAACTCACACATGC 779

Qy        712 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 839

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 899

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 959

Qy        892 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 951
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Db        960 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1019

Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
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Db       1020 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1079

Qy       1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1080 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1139

Qy       1072 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
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Db       1140 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1199

Qy       1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
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Db       1200 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1259

Qy       1192 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1319

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1379

Qy       1312 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
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Db       1380 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1439

Qy       1372 AAATGA 1377
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RESULT 15
US-10-909-011-1
; Sequence 1, Application US/10909011
; Publication No. US20050112061A1
; GENERAL INFORMATION:
;  APPLICANT: Jocelyn Holash
;  APPLICANT:  George Yancopoulos
;  APPLICANT:  Phyllis R. Wachsberger
;  APPLICANT:  Adam P. Dicker
;  APPLICANT:  Randy Burd
;  TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
;  FILE REFERENCE: REG 716A
;  CURRENT APPLICATION NUMBER: US/10/909,011
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: 60/492,864
;  PRIOR FILING DATE: 2003-08-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1453
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-909-011-1

  Query Match             96.5%;  Score 1328.4;  DB 21;  Length 1453;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1367;  Conservative    0;  Mismatches    1;  Indels   18;  Gaps    2;

Qy          1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128

Qy         61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
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Qy        121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
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Qy        181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240
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Qy        301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
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Db        420 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 479

Qy        421 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480
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Db        480 TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 539

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Db        540 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 599

Qy        541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600
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Db        600 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 659

Qy        601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
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Db        660 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719
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Qy        661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAG---------GACAAAACTCACACATGC 711
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Db        720 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGGCCCGGGCGACAAAACTCACACATGC 779

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Db        780 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 839

Qy        772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 831
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Db        840 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 899

Qy        832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 891
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Qy        952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011
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Db       1200 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1259

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Db       1260 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1319

Qy       1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
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Qy       1372 AAATGA 1377
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Job time : 937 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 23, 2005, 15:40:31 ; Search time 120 Seconds
(without alignments)
1954.436 Million cell updates/sec

Title: US-10-811-170-2
Perfect score: 2437
Sequence: 1 MVSYWDTGVLLCALLSCLLL.....MHEALHNHYTQKSLSLSPGK 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1267.5	52.0	466	2	Q6IN78	Q6in78 homo sapien
2	1253.5	51.4	487	2	Q65ZL2	Q65zl2 mus sp. fv/
3	1252.5	51.4	472	2	Q6N089	Q6n089 homo sapien
4	1252	51.4	470	2	Q6PJA4	Q6pja4 homo sapien
5	1246.5	51.1	475	2	Q6MZQ6	Q6mzq6 homo sapien
6	1246	51.1	478	2	Q6PI81	Q6pi81 homo sapien
7	1245.5	51.1	465	2	Q6GMX6	Q6gmx6 homo sapien
8	1245	51.1	476	2	Q6GMX1	Q6gmx1 homo sapien
9	1244.5	51.1	475	2	Q6GMW7	Q6gmw7 homo sapien
10	1242.5	51.0	482	2	Q7Z351	Q7z351 homo sapien
11	1240.5	50.9	330	1	GC1_HUMAN	P01857 homo sapien
12	1240.5	50.9	469	2	Q7Z7P5	Q7z7p5 homo sapien
13	1240.5	50.9	470	2	Q7Z5W1	Q7z5w1 homo sapien
14	1239.5	50.9	473	2	Q6MZV7	Q6mzv7 homo sapien
15	1237.5	50.8	348	2	Q6PYX1	Q6pyx1 homo sapien
16	1237.5	50.8	480	2	Q6PJF1	Q6pjf1 homo sapien
17	1236.5	50.7	473	2	Q6P055	Q6p055 homo sapien
18	1236.5	50.7	480	2	Q6N094	Q6n094 homo sapien
19	1236.5	50.7	481	2	Q6N097	Q6n097 homo sapien
20	1235	50.7	466	2	Q6N096	Q6n096 homo sapien
21	1233	50.6	679	2	Q96PQ8	Q96pq8 homo sapien
22	1229.5	50.5	475	2	Q6N095	Q6n095 homo sapien
23	1229.5	50.5	544	2	Q6PJ95	Q6pj95 homo sapien
24	1155	47.4	464	2	Q6MZU6	Q6mzu6 homo sapien
25	1150	47.2	417	2	Q6N093	Q6n093 homo sapien
26	1149.5	47.2	518	2	Q6N030	Q6n030 homo sapien
27	1148.5	47.1	326	1	GC2_HUMAN	P01859 homo sapien
28	1146.5	47.0	465	2	Q6P6C4	Q6p6c4 homo sapien
29	1146	47.0	354	2	Q86TT2	Q86tt2 homo sapien
30	1144	46.9	327	1	GC4_HUMAN	P01861 homo sapien
31	1144	46.9	473	2	Q8TC63	Q8tc63 homo sapien
32	1142	46.9	521	2	Q8N4Y9	Q8n4y9 homo sapien
33	1135	46.6	476	2	Q6MZX7	Q6mzx7 homo sapien
34	1134.5	46.6	493	2	Q68CN4	Q68cn4 homo sapien
35	1131	46.4	509	2	Q8NF17	Q8nf17 homo sapien
36	1126	46.2	290	1	GC3_HUMAN	P01860 homo sapien
37	925.5	38.0	323	1	GC_RABIT	P01870 oryctolagus
38	917	37.6	337	2	Q95M34	Q95m34 equus cabal
39	900	36.9	329	1	GC2_CAVPO	P01862 cavia porce
40	872	35.8	470	2	Q7TMK1	Q7tmk1 mus musculu
41	866.5	35.6	329	1	GC3_MOUSE	P22436 mus musculu
42	855.5	35.1	398	1	GC3M_MOUSE	P03987 mus musculu
43	854	35.0	464	2	Q6PIP8	Q6pip8 mus musculu
44	851	34.9	458	2	Q65ZQ1	Q65zq1 homo sapien
45	847.5	34.8	463	2	Q99LC4	Q99lc4 mus musculu

ALIGNMENTS

RESULT 1
Q6IN78
ID Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

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DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   466 AA;  50853 MW;  53EB0BCEDE81076E CRC64;

  Query Match             52.0%;  Score 1267.5;  DB 2;  Length 466;
  Best Local Similarity   55.8%;  Pred. No. 8.3e-80;
  Matches  281;  Conservative   34;  Mismatches  104;  Indels   85;  Gaps   16;

Qy          2 VSYWDTGVLLCALL---SCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRV 58
              : :| : | | |:|    | :   | |                 : |  | : |
Db          1 MEFWLSWVFLVAILKGVQCEVQLVESGGG----------------LIQPGGSLTLSCAA 43

Qy         59 T----SPNITVTLKKFPLDTLIPDGKRIIW-------------DSRKG-FIIS-----NA 95
              :    | |    ::: |       || : |             || || | ||     |
Db         44 SGLTVSSNYMHWVRQAP-------GKGLEWVSVLYIGGATYYADSVKGRFTISRDNSKNT 96

Qy         96 TYKEIGLLTCEATVNGHLYKTNYLTHRQ---TNTIIDV-----------VLSPSHGIELS 141
              | ::  |  | |   :  : ||:         |:: |           |:||   : :
Db         97 LYLQMNSLRAEDTAVYYCARGNYVVPAAPWGQGTLVTVSSASTKGPSVFPLAPSS--KST 154

Qy        142 VGEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
              |    | |  :      :  :|      |  |    ::         | :    | :|:
Db        155 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL-------QSSGLYSLSSVVTV 207

Qy        199 DGVTRSDQGLYTCAASSGLMTKKNSTFV--RVHEK--DKTHTCPPCPAPELLGGPSVFLF 254
                 :   |  | |  :     | ::| |  ||  |  ||||||||||||||||||||||
Db        208 PSSSLGTQ-TYICNVNH----KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLF 262

Qy        255 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 322

Qy        315 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV 382

Qy        375 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 442

Qy        435 SCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||
Db        443 SCSVMHEALHNHYTQKSLSLSPGK 466


RESULT 2
Q65ZL2
ID   Q65ZL2      PRELIMINARY;      PRT;   487 AA.
AC   Q65ZL2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   FV/M4.
GN   Name=M4-IFN-<tau>;
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96272580; PubMed=8688499;
RA   Qi Y., Xiang J.;
RT   "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT   antibody secreted from myeloma cells.";
RL   Hum. Antibodies Hybridomas 6:161-166(1995).
DR   EMBL; S82493; AAB37424.2; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   487 AA;  53578 MW;  C7BAB69F30555504 CRC64;

  Query Match             51.4%;  Score 1253.5;  DB 2;  Length 487;
  Best Local Similarity   64.5%;  Pred. No. 8.2e-79;
  Matches  260;  Conservative   29;  Mismatches   67;  Indels   47;  Gaps   10;

Qy         93 SNATYKEIGLLTCEATVNGHLYKTNYLTH-RQTNTI-------------------IDVVL 132
              |:  | ::  || | :    :  | :|  |   |  |:                   | :
Db         95 SSTAYMQLNSLTSEDSA-VYFCKRSYYGHWGQGTTLTGSGGGGSGGGGSGGGGSRIQMTQ 153

Qy        133 SPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLV------------NRD 180
              ||:  : :|||| : : |  |    |:  :  | |   : :  :|:             :|
Db        154 SPA-SLSVSVGELVTITC--RASENIYSNLAW-YQQKQGKSPQLLVYAATNLADGVPSRF 209

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGL-MTKKNSTFVRVHEK----DKTH 235
                : ||::      :| |: :   | | | |     |   |     | : :  :    ||||
Db        210 SGSGSGTQY-----SLKINSLQSEDFGSYYCQHFWGTPYTFGGGTRLEIKPRSKSCDKTH 264

Qy        236 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 295
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 TCPPGPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 324

Qy        296 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 355
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        325 HNAKTKPREEQYNSTYRVFSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 384

Qy        356 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 444

Qy        416 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||
Db        445 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 487


RESULT 3
Q6N089
ID   Q6N089      PRELIMINARY;      PRT;   472 AA.
AC   Q6N089;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   Name=DKFZp686P15220;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
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DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match           51.4%;  Score 1252.5;  DB 2;  Length 472;
  Best Local Similarity   59.1%;  Pred. No. 9.3e-79;
  Matches  273;  Conservative   24;  Mismatches   90;  Indels   75;  Gaps   14;

Qy         49 GRELVIPCRVTSPNITVTLKKFPLDTLI------PDGKRIIW--------------DSRK 88
              || | : | :           | |           || : |              || |
Db         34 GRSLRLSCAASG---------FTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAYADSVK 84

Qy         89 G-FIIS-----NATYKEIGLLTCEATV-----------NGHLYKTNYLTHRQTNTIIDV- 130
              | | ||     |: | ::  |  | |           | : |  :       | |:
Db         85 GRFTISRDNGKNSLYLQMNSLRAEDTALYYCAKEIGAHNFYYYGMDVWGQGTTVTVSSAS 144

Qy        131 -------VLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRD 180
                    |:||   : : |     | |  :      :  :|      |  |    ::
Db        145 TKGPSVFPLAPSS--KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL--- 199

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFV--RVHEK--DKTHT 236
                  |  :    | :|:   :    |  | |  :     | ::| |  ||  |  |||||
Db        200 ----QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNH----KPSNTKVDKRVEPKSCDKTHT 250

Qy        237 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 310

Qy        297 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 370

Qy        357 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 430

Qy        417 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||
Db        431 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 4
Q6PJA4
ID   Q6PJA4      PRELIMINARY;      PRT;   470 AA.
AC   Q6PJA4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51715 MW;  7B49556A11FD7D99 CRC64;

  Query Match           51.4%;  Score 1252;  DB 2;  Length 470;
  Best Local Similarity   62.4%;  Pred. No. 1e-78;
  Matches  262;  Conservative   23;  Mismatches   85;  Indels   50;  Gaps    9;

Qy         79 GKRIIW--------------DSRKG-FIIS-----NATYKEIGLLTCEATV------NGH 112
              || : |              || || | ||      |: | ::  |  | |       :|
Db         61 GKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGS 120

Qy        113 LYKTNYLTHRQTNTIIDV-----------VLSPSHGIELSVGEKLVLNCTARTELNVGID 161
                :  ::       |:: |           |:||   : : |     | |  :      :
Db        121 SWYRDWFDPWGQGTLVTVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLVKDYFPEPVT 178

Qy        162 FNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLM 218
                :|      |  |    ::         | :    | :|:   :    |  | |  :
Db        179 VSWNSGALTSGVHTFPAVL-------QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNHKPS 230

Qy        219 TKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 278
                |    |      ||||||||||||||||||||||||||||||||||||||||||||||
Db        231 NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 290

Qy        279 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 350

Qy        339 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 410

Qy        399 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 5
Q6MZQ6
ID   Q6MZQ6      PRELIMINARY;      PRT;   475 AA.
AC   Q6MZQ6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686G11190.
GN   Name=DKFZp686G11190;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
```

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RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA   Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640947; CAE45972.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  52043 MW;  B7EAE255A26F4B8E CRC64;

  Query Match             51.1%;  Score 1246.5;  DB 2;  Length 475;
  Best Local Similarity   61.0%;  Pred. No. 2.4e-78;
  Matches  258;  Conservative   26;  Mismatches   88;  Indels   51;  Gaps    8;

Qy         79 GKRIIW--------------DSRKG-FIIS-----NATYKEIGLLTCEATVNGHLYKTNY 118
              || : |              || || | ||     | | ::  |  : |   :  : :|
Db         61 GKGLEWVSGISSSGVNTYYADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADY 120

Qy        119 LTHRQT-----------NTIIDVVLSPSHGIEL---------SVGEKLVLNCTARTELNV 158
                :: :            |:: |  : : |  :         : |    | |  :
Db        121 RDYQVSPAYWYFDVWGRGTLVSVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 180

Qy        159 GIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASS 215
               :  :|     |  |    ::        | :    | :|:   :   |  | |  :
Db        181 PVTVSWNSGALTSGVHTFPAVL-------QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNH 232

Qy        216 GLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 275
                |    |     ||||||||||||||||||||||||||||||||||||||||||||||
Db        233 KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 292

Qy        276 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 352

Qy        336 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 412

Qy        396 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLS 472

Qy        456 PGK 458
              |||
Db        473 PGK 475


RESULT 6
Q6PI81
ID   Q6PI81      PRELIMINARY;      PRT;   478 AA.
AC   Q6PI81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC041037; AAH41037.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   478 AA;  52666 MW;  17BED38D917970D6 CRC64;

  Query Match             51.1%;  Score 1246;  DB 2;  Length 478;
  Best Local Similarity   61.6%;  Pred. No. 2.7e-78;
  Matches  265;  Conservative   23;  Mismatches   80;  Indels   62;  Gaps   11;

Qy         79 GKRIIW--------------DSRKG-FIIS-----NATYKEIGLLTCE------------ 106
              || : |              || || | ||     |: | ::  |  |
Db         61 GKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFE 120

Qy        107 ---ATVNGHLY--------KTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTE 155
                 |||   |         |  :|    :|    |   :   : : |    | |  :
Db        121 STMTTVNADYYYFYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180

Qy        156 LNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCA 212
                  :  :|     |  |    ::        | :    | :|:   :   |  | |
Db        181 FPEPVTVSWNSGALTSGVHTFPAVL-------QSSGLYSLSSVVTVPSSSLGTQ-TYICN 232

Qy        213 ASSGLMTKKNSTFV--RVHEK--DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP 268
               :     | ::| |  ||  |  ||||||||||||||||||||||||||||||||||||
Db        233 VNH----KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP 288

Qy        269 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK 348

Qy        329 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI 388
              ||||||||||||||||||||||||||||||||||||:|:||||||||||||||||||||
Db        349 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI 408

Qy        389 AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT 468
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Qy        449 QKSLSLSPGK 458
              ||||||||||
Db        469 QKSLSLSPGK 478


RESULT 7
Q6GMX6
ID   Q6GMX6      PRELIMINARY;      PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073766; AAH73766.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51083 MW;  B3A9B7D0FDB1386E CRC64;

  Query Match           51.1%;  Score 1245.5;  DB 2;  Length 465;
  Best Local Similarity   61.9%;  Pred. No. 2.8e-78;
  Matches  258;  Conservative   23;  Mismatches   91;  Indels   45;  Gaps    7;

Qy         77 PDGKRIIWDSR---KGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQT--------- 124
              | || : |  |    |    | : |    :: : : |    | : :|  |
Db         59 PAGKGLEWIGRIYTSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARGR 118

Qy        125 ---------NTIIDV-----------VLSPSHGIELSVGEKLVLNCTARTELNVGIDFNW 164
                      |:: |            |:||   : : |    | |  :      :  :|

Db        119 FTYFDYWGQGTLVTVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLVKDYFPEPVTVSW 176

Qy        165 E---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKK 221
                  |  |    ::      | :   | :|:   :   |  | |  :    |
Db        177 NSGALTSGVHTFPAVL-------QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNHKPSNTK 228

Qy        222 NSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 281
                  |     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 288

Qy        282 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 348

Qy        342 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 408

Qy        402 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 8
Q6GMX1
ID   Q6GMX1      PRELIMINARY;      PRT;   476 AA.
AC   Q6GMX1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073773; AAH73773.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
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DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   476 AA;  52286 MW;  622AABA5C62DDE9D CRC64;

  Query Match             51.1%;  Score 1245;  DB 2;  Length 476;
  Best Local Similarity   60.8%;  Pred. No. 3.1e-78;
  Matches  261;  Conservative   23;  Mismatches   85;  Indels   60;  Gaps    9;

Qy         77 PDGKRIIWDSRKGFI-ISNATYKEIGL-----LTCEATVNGHLYKTNYLTHRQT------ 124
              | || : |    |:|  | :||    |     :: : : |    | | :|   |
Db         61 PPGKGLEW---IGYIYYSGSTYYNPSLKSRVTISLDTSKNQFSLKMNSVTAADTAVYFCA 117

Qy        125 ---------------------NTIIDV-----------VLSPSHGIELSVGEKLVLNCTA 152
                                   |:: |           |:||   : : |    | |
Db        118 RAGVWGSFRSWAIDGFNIWGQGTMVTVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLV 175

Qy        153 RTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLY 209
              :      :  :|      | |    ::        | :    | :|:   :   |  |
Db        176 KDYFPEPVTVSWNSGALTSGVHTFPAVL-------QSSGLYSLSSVVTVPSSSLGTQ-TY 227

Qy        210 TCAASSGLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE 269
              |  :      |    |      ||||||||||||||||||||||||||||||||||||
Db        228 ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE 287

Qy        270 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 347

Qy        330 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 407

Qy        390 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 467

Qy        450 KSLSLSPGK 458
              |||||||||
Db        468 KSLSLSPGK 476


RESULT 9
Q6GMW7
ID   Q6GMW7      PRELIMINARY;      PRT;   475 AA.
AC   Q6GMW7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073782; AAH73782.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  51987 MW;  2A1FE55D736860F8 CRC64;

  Query Match             51.1%;  Score 1244.5;  DB 2;  Length 475;
  Best Local Similarity   64.4%;  Pred. No. 3.4e-78;
  Matches  261;  Conservative   19;  Mismatches   84;  Indels   41;  Gaps    9;

Qy         85 DSRKG-FIIS-----NATYKEIGLLTCE---------ATVNG----HLYKTNYLTHRQTN 125
              || || | ||     |  | ::| |  |         |   |    : |    :  : |
Db         81 DSVKGRFTISRDNYKNTLYLQLGSLRAEDKAVYYCARARCRGDTCLNFYYGLDVWGQGTT 140

Qy        126 TIIDVV---------LSPSHGIELSVGEKLVLNCTARTELNVGIDFNWE---YPSSKHQH 173
               |:           |:||   : : |    | |  :      :  :|      | |
Db        141 VIVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 198

Qy        174 KKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDK 233
              ::          | :    | :|:   :   |  | |  :      |    |      ||
Db        199 PAVL-------QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNHKPSNTKVDKKVEPKSCDK 250

Qy        234 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 310

Qy        294 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 370

Qy        354 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 430

Qy        414 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||||
Db        431 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475


RESULT 10
Q7Z351
ID   Q7Z351      PRELIMINARY;      PRT;   482 AA.
AC   Q7Z351;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein DKFZp686N02209.
GN   Name=DKFZp686N02209;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX538118; CAD98026.1; -.
DR   HSSP; P01857; 1HZH.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   482 AA;  52852 MW;  EDA75F1901D1A034 CRC64;

  Query Match             51.0%;  Score 1242.5;  DB 2;  Length 482;
  Best Local Similarity   57.1%;  Pred. No. 4.7e-78;
  Matches  266;  Conservative   27;  Mismatches  100;  Indels   73;  Gaps   10;

Qy         49 GRELVIPCRVT----SPNITVTLKKFPLDTLIPDGKRIIW-------------DSRKG- 89
              || | : |  :    | :    |:: |       || : |               || ||
Db         34 GRSLRLSCIASGFSFSGSAMHWLRQIP-------GKGLEWVAVISYDGNHKLYSDSVKGR 86

Qy         90 FIISNATYKEIGLLTCEATVNGH--LYKTNYLTHRQTNTIIDVV---------------- 131
              | ||    | :  |   :  :    :|      | :| :|  ::
Db         87 FTISRDNSKSLLFLHVNSLTSADTAIYYCARDFHSKTTSIFGLIPLYFYYSAMDTWGRGT 146

Qy        132 ---------------LSPSHGIELSVGEKLVLNCTARTELNVGIDFNWE---YPSSKHQ 172
                            |:||   : : |   | |  :      :  :|       |   |
Db        147 TVIVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 204

Qy        173 HKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKD 232
                ::          | :    | :|:   :   |  | |  :       |     |     |
Db        205 FPAVL-------QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNHKPSNTKVDKKVEPKSCD 256

Qy        233 KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 316

Qy        293 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 376

Qy        353 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 436

Qy        413 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              ||||||||||||||||||||||||| ||||||||||||||||
Db        437 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 482


RESULT 11
GC1_HUMAN
ID   GC1_HUMAN      STANDARD;      PRT;   330 AA.
AC   P01857;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig gamma-1 chain C region.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82274238; PubMed=6287432;
RA   Ellison J.W., Berson B.J., Hood L.E.;
RT   "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL   Nucleic Acids Res. 10:4071-4079(1982).
RN   [2]
RP   SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [3]
RP   SEQUENCE OF 136-329 (EU).
RX   MEDLINE=71064025; PubMed=5530842;
RA   Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA   Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL   Biochemistry 9:3171-3181(1970).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN NIE).
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT   peptides of the H-chain, alignment of the tryptic peptides and
RT   discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [5]
RP   SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC       G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC       G1M(3) marker and the G1M (non-1) markers.
CC   -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC       116, 198, 269 and 272.
CC   -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC       155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC       268-272.
CC   -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC       residues 198, 267 and 272.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GHHU.
DR   PDB; 1AJ7; X-ray; H=1-103.
DR   PDB; 1D5B; X-ray; B/H=1-101.
DR   PDB; 1D5I; X-ray; H=1-101.
DR   PDB; 1D6V; X-ray; H=1-101.
DR   PDB; 1DN2; X-ray; A/B=120-326.
DR   PDB; 1E4K; X-ray; A/B=106-329.
DR   PDB; 1FC1; X-ray; A/B=106-329.
DR   PDB; 1FC2; X-ray; D=106-329.
DR   PDB; 1FCC; X-ray; A=121-326.
DR   PDB; 1HZH; X-ray; H/K=1-330.
DR   PDB; 1I7Z; X-ray; B/D=1-103.
DR   PDB; 1IIS; X-ray; A/B=107-330.
DR   PDB; 1IIX; X-ray; A/B=107-330.
DR   PDB; 1L6X; X-ray; A=120-326.
DR   PDB; 1OQX; X-ray; A/B=119-330.
DR   PDB; 2RCS; X-ray; H=1-103.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   3D-structure; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin C region; Immunoglobulin domain.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       Hinge.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       Interchain (with light chain).
FT   DISULFID    109    109       Interchain (with heavy chain).
FT   DISULFID    112    112       Interchain (with heavy chain).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   CARBOHYD    180    180       N-linked (GlcNAc. . .).
FT   VARIANT      97     97       K -> R (in G1M(3) marker).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (in G1M(non-1) marker).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (in G1M(non-1) marker).
FT                                /FTId=VAR_003888.
FT   STRAND       23     24
FT   STRAND       26     33
FT   STRAND       38     38
FT   STRAND       41     41
FT   TURN         42     45
FT   TURN         48     49
FT   STRAND       50     52
FT   STRAND       57     58
FT   TURN         59     61
FT   STRAND       62     71
FT   HELIX        73     75
FT   TURN         76     78
FT   STRAND       82     87
FT   TURN         88     91
FT   STRAND       92     97
FT   TURN        102    103
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    149
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    167
FT   STRAND      171    172
FT   STRAND      176    177
FT   TURN        179    180
FT   STRAND      183    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      261    266
FT   TURN        267    268
FT   STRAND      269    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      306    311
FT   TURN        313    314
FT   HELIX       316    318
FT   STRAND      319    324
SQ   SEQUENCE   330 AA;  36106 MW;  3770EE106C2FA33D CRC64;

  Query Match             50.9%;  Score 1240.5;  DB 1;  Length 330;
  Best Local Similarity   86.4%;  Pred. No. 4e-78;
  Matches  242;  Conservative    7;  Mismatches   12;  Indels   19;  Gaps    5;

Qy        197 TIDGVTRSDQGLYTCAA-----SSGLMT---------KKNSTFV--RVHEK--DKTHTCP 238
              |   | :|  |||: ::     || | |         | ::| |  :|  |  |||||||
Db         52 TFPAVLQS-SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP 110

Qy        239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 170

Qy        299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 230

Qy        359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 290

Qy        419 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        291 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 12
Q7Z7P5
ID   Q7Z7P5      PRELIMINARY;      PRT;   469 AA.
AC   Q7Z7P5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHG1 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC051328; AAH51328.1; -.
DR   HSSP; P01857; 1HZH.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   469 AA;  51395 MW;  C8D5BE12BAAF795C CRC64;

  Query Match            50.9%;  Score 1240.5;  DB 2;  Length 469;
  Best Local Similarity   86.4%;  Pred. No. 6.3e-78;
  Matches  242;  Conservative    7;  Mismatches   12;  Indels   19;  Gaps    5;

Qy        197 TIDGVTRSDQGLYTCAA-----SSGLMT---------KKNSTFV--RVHEK--DKTHTCP 238
              |   | :|  |||: ::     || | |         | ::| |  :|  |  |||||||
Db        191 TFPAVLQS-SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP 249

Qy        239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 309

Qy        299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 369

Qy        359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 429

Qy        419 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        430 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469


RESULT 13
Q7Z5W1
ID   Q7Z5W1      PRELIMINARY;      PRT;   470 AA.
AC   Q7Z5W1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053984; AAH53984.1; -.
DR   HSSP; P01857; 1HZH.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51204 MW;  778CF34521483E1A CRC64;

  Query Match            50.9%;  Score 1240.5;  DB 2;  Length 470;
  Best Local Similarity   86.4%;  Pred. No. 6.3e-78;
  Matches  242;  Conservative    7;  Mismatches   12;  Indels   19;  Gaps    5;

Qy        197 TIDGVTRSDQGLYTCAA-----SSGLMT---------KKNSTFV--RVHEK--DKTHTCP 238
              |   | :|  |||: ::     || | |         | ::| |  :|  |  |||||||
Db        192 TFPAVLQS-SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP 250

Qy        239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 310

Qy        299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 370

Qy        359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 430

Qy        419 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        431 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 14
Q6MZV7
ID   Q6MZV7      PRELIMINARY;      PRT;   473 AA.
AC   Q6MZV7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
```

```
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686C11235.
GN   Name=DKFZp686C11235;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human small intestine;
RG   The German Human cDNA Consortium;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640853; CAE45920.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  52121 MW;  9476EAE4C0BFC447 CRC64;

  Query Match             50.9%;  Score 1239.5;  DB 2;  Length 473;
  Best Local Similarity   61.6%;  Pred. No. 7.5e-78;
  Matches  263;  Conservative   25;  Mismatches   78;  Indels   61;  Gaps   11;

Qy          79 GKRIIW--------------DSRKG-FIIS-----NATYKEIGLLTCEATVNGHLYKTNY 118
               || : |              || :| | ||     |: | ::  |  | |  :  : |
Db          61 GKGLEWLSYITRSGNTVYYADSLQGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARQNE 120

Qy         119 LTHRQTNTIID--------------------VVLSPSHGIELSVGEKLVLNCTARTELNV 158
                |     :  |                   |:||   : : |    | |  :
Db         121 HTSPWYPSFFDYWGQGILVTVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLVKDYFLE 178

Qy         159 GIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASS 215
                :  :|      | |    ::         | :    | :|:   :   |  | |  :
Db         179 PVTVSWNSGALTSGVHTFPAVL-------QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNH 230

Qy         216 GLMTKKNSTFV--RVHEK--DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 271
                   | ::| |  ||  |  ||||||||||||||||||||||||||||||||||||||||
Db         231 ----KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 286

Qy         272 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 331
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         287 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 346

Qy         332 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 391
               |||||||||||||||||||||||||||||||||:|:||||||||||||||||||||||
Db         347 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE 406

Qy         392 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 451
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         407 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 466

Qy         452 LSLSPGK 458
               |||||||
Db         467 LSLSPGK 473


RESULT 15
Q6PYX1
ID   Q6PYX1      PRELIMINARY;      PRT;   348 AA.
AC   Q6PYX1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hepatitis B virus receptor binding protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhu N.S., Chen Y.Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY570731; AAS88328.1; -.
DR   HSSP; P01857; 1AJ7.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   348 AA;  38162 MW;  DD96C3D7E0BE5845 CRC64;

  Query Match             50.8%;  Score 1237.5;  DB 2;  Length 348;
  Best Local Similarity   86.1%;  Pred. No. 7e-78;
  Matches  241;  Conservative    8;  Mismatches   12;  Indels   19;  Gaps    5;

Qy         197 TIDGVTRSDQGLYTCAA-----SSGLMT---------KKNSTFV--RVHEK--DKTHTCP 238
               |   | :|  |||: ::      || | |         | ::| |  ||  |  |||||||
Db          70 TFPAVLQS-SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP 128

Qy         239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         129 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 188

Qy         299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         189 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 248

Qy         359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 418
               ||||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||
Db         249 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 308

Qy         419 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
               |||||||||||||||||||||||||||||||||||||||
Db         309 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 348


Search completed: September 23, 2005, 17:17:04
Job time : 124 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 23, 2005, 14:00:46 ; Search time 120 Seconds
(without alignments)
1476.135 Million cell updates/sec

Title: US-10-811-170-2
Perfect score: 2437
Sequence: 1 MVSYWDTGVLLCALLSCLLL.....MHEALHNHYTQKSLSLSPGK 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2437	100.0	458	4	AAY97596	Aay97596 Flt1 rece
2	2437	100.0	458	5	ABP52449	Abp52449 Modified
3	2399	98.4	458	4	AAY97594	Aay97594 Flt1 rece
4	2399	98.4	458	5	ABP52447	Abp52447 Modified
5	2275.5	93.4	432	5	ABP52450	Abp52450 Flt1D2.Fl
6	2069.5	84.9	455	4	AAY97595	Aay97595 Flt1 rece
7	2069.5	84.9	455	5	ABP52448	Abp52448 Modified
8	2049	84.1	462	4	AAY97592	Aay97592 Flt1 rece
9	2049	84.1	462	5	ABP52445	Abp52445 Mutation
10	2038	83.6	452	4	AAY97591	Aay97591 Flt1 rece
11	2038	83.6	452	5	ABP52444	Abp52444 Mutation
12	2015.5	82.7	567	4	AAY97593	Aay97593 Flt1 rece
13	2015.5	82.7	567	5	ABP52446	Abp52446 Mutation
14	2014.5	82.7	567	4	AAY97597	Aay97597 Flt1 rece
15	2014.5	82.7	567	5	ABP52442	Abp52442 Flt1(1-3)
16	2003.5	82.2	557	4	AAY97590	Aay97590 Flt1 rece
17	2003.5	82.2	557	5	ABP52443	Abp52443 Mutation
18	1726.5	70.8	934	6	ABP70840	Abp70840 MVP-B pro
19	1716	70.4	949	6	ABP70841	Abp70841 MVP-C pro
20	1627.5	66.8	816	6	ABP70853	Abp70853 MVP-A pro
21	1619.5	66.5	810	6	ABP70839	Abp70839 MVP-A pro
22	1304	53.5	680	2	AAR48037	Aar48037 tICAM(453
23	1304	53.5	680	6	ABU07273	Abu07273 Human exp
24	1293.5	53.1	915	7	ABW02188	Abw02188 Human IL-
25	1292	53.0	640	8	ADP76035	Adp76035 AMIGO pol
26	1290.5	53.0	388	6	ADA14289	Ada14289 Mutated M
27	1290.5	53.0	915	7	ABW02191	Abw02191 Human IL-
28	1289.5	52.9	388	5	ABB07681	Abb07681 MOG-Fc fu
29	1289.5	52.9	388	6	ADA14265	Ada14265 Human imm
30	1289.5	52.9	555	8	ADI03928	Adi03928 B7-L1-Ig
31	1288	52.9	900	7	ABW02182	Abw02182 Human IL-
32	1285.5	52.7	609	8	ADP76033	Adp76033 AMIGO pol
33	1284.5	52.7	731	8	ADQ07407	Adq07407 hCBE11/hB
34	1284.5	52.7	731	8	ADQ12184	Adq12184 huCBE11/h
35	1284.5	52.7	735	8	ADQ07411	Adq07411 hCBE11 mo
36	1284.5	52.7	735	8	ADQ12188	Adq12188 huCBE11 m
37	1281.5	52.6	594	4	AAU09817	Aau09817 Murine FG
38	1281.5	52.6	900	7	ABW02185	Abw02185 Human IL-
39	1280	52.5	497	3	AAY97172	Aay97172 Human FGF
40	1279.5	52.5	622	3	AAY97170	Aay97170 Human FGF
41	1279	52.5	581	8	ADP03590	Adp03590 Infection
42	1279	52.5	631	7	ADH34696	Adh34696 CE7-speci
43	1277.5	52.4	489	5	AAO19052	Aao19052 Cell adhe
44	1275.5	52.3	910	3	AAY92206	Aay92206 Fusion po
45	1275.5	52.3	910	7	ABW02179	Abw02179 Human cyt

ALIGNMENTS

RESULT 1
AAY97596
ID AAY97596 standard; protein; 458 AA.
XX
AC AAY97596;
XX
DT 05-APR-2001 (first entry)
XX
DE Flt1 receptor fusion protein VEGFR1R2-FcDeltaC1(a).
XX
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IgG Fc region.
XX
OS Unidentified.
XX
PN WO200075319-A1.
XX
PD 14-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US014142.
XX
PR 08-JUN-1999; 99US-0138133P.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Papadopoulos NJ, Davis S, Yancopoulos GD;
XX
DR WPI; 2001-071076/08.
DR N-PSDB; AAA91076.
XX
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model
PT systems.
XX
PS Claim 49; Fig 24; 159pp; English.
XX
CC This sequence represents a fusion protein of the invention between the
CC Flt1 receptor and the Fc region of IgG. The specification relates to
CC modified chimeric polypeptides with improved pharmacokinetics. The
CC modified chimeric polypeptides are preferably Flt1 receptor polypeptides
CC that have been modified to improve their pharmacokinetic profile. The
CC polypeptides can be used to decrease or inhibit plasma leakage and/or
CC vascular permeability in a mammal
XX
SQ Sequence 458 AA;

Query Match 100.0%; Score 2437; DB 4; Length 458;

```
  Best Local Similarity   100.0%;  Pred. No. 1.1e-153;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||
Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 2
ABP52449
ID   ABP52449 standard; protein; 458 AA.
XX
AC   ABP52449;
XX
DT   23-OCT-2002  (first entry)
XX
DE   Modified Flt1 receptor VEGFR1R2-FcDELTAC1(a) protein sequence.
XX
KW   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW   psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW   vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW   ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW   brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW   kidney disease; eye disorder; age-related macular degeneration;
KW   diabetic retinopathy.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200260489-A1.
XX
PD   08-AUG-2002.
XX
PF   28-JAN-2002; 2002WO-US002466.
XX
PR   31-JAN-2001; 2001US-00773877.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Xia Y,  Rudge JS,  Yancopoulos GD;
XX
DR   WPI; 2002-608488/65.
DR   N-PSDB; ABQ74610.
XX
PT   Treating psoriasis and enhancing wound healing in humans comprises the
PT   administration of a vascular endothelial cell growth factor (VEGF)
PT   antagonist.
XX
PS   Example 20; Fig 24A-C; 179pp; English.
XX
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence represents VEGFR1R2-
CC   FcDELTAC1(a) which is used in an example from the present invention
XX
SQ   Sequence 458 AA;

  Query Match             100.0%;  Score 2437;  DB 5;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-153;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||
Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 3
AAY97594
ID   AAY97594 standard; protein; 458 AA.
XX
AC   AAY97594;
XX
DT   05-APR-2001  (first entry)
XX
DE   Flt1 receptor fusion protein Flt1D2.Flk1D3.FcDeltaC1(a).
XX
KW   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW   plasma leakage; vascular permeability; IgG Fc region.
```

XX
OS Unidentified.
XX
PN WO200075319-A1.
XX
PD 14-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US014142.
XX
PR 08-JUN-1999; 99US-0138133P.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Papadopoulos NJ, Davis S, Yancopoulos GD;
XX
DR WPI; 2001-071076/08.
DR N-PSDB; AAA91074.
XX
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model
PT systems.
XX
PS Claim 49; Fig 21; 159pp; English.
XX
CC This sequence represents a fusion protein of the invention between the
CC Flt1 receptor and the Fc region of IgG. The specification relates to
CC modified chimeric polypeptides with improved pharmacokinetics. The
CC modified chimeric polypeptides are preferably Flt1 receptor polypeptides
CC that have been modified to improve their pharmacokinetic profile. The
CC polypeptides can be used to decrease or inhibit plasma leakage and/or
CC vascular permeability in a mammal
XX
SQ Sequence 458 AA;

Query Match 98.4%; Score 2399; DB 4; Length 458;
Best Local Similarity 98.7%; Pred. No. 3.9e-151;
Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

```
Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        178 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC 237

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
```

RESULT 4

ABP52447
ID ABP52447 standard; protein; 458 AA.
XX
AC ABP52447;
XX
DT 23-OCT-2002 (first entry)
XX
DE Modified Flt1 receptor Flt1D2.Flk1D3.FcDELTAC1(a) protein sequence.
XX
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW kidney disease; eye disorder; age-related macular degeneration;
KW diabetic retinopathy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200260489-A1.
XX
PD 08-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002466.
XX
PR 31-JAN-2001; 2001US-00773877.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Xia Y, Rudge JS, Yancopoulos GD;
XX
DR WPI; 2002-608488/65.
DR N-PSDB; ABQ74608.
XX
PT Treating psoriasis and enhancing wound healing in humans comprises the
PT administration of a vascular endothelial cell growth factor (VEGF)
PT antagonist.
XX
PS Example 17; Fig 21A-C; 179pp; English.
XX
CC The present invention describes a method for treating psoriasis and
CC enhancing wound healing in a mammal or a human. The method comprises
CC administering a vascular endothelial cell growth factor (VEGF) antagonist
CC to the mammal or human. A VEGF antagonist has antipsoriatic,
CC antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC nephrotropic and ophthalmological activities. The method can be used in
CC treating psoriasis and enhancing wound healing in humans by administering
CC VEGF antagonist. The method is also useful in treating clinical
CC conditions characterised by vascular permeability, oedema or
CC inflammation, such as brain oedema associated with injury, oedema
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC asthma, burns, kidney diseases, or eye disorders such as age-related
CC macular degeneration and diabetic retinopathy. The method may also be
CC used in making the polypeptide to decrease or inhibit plasma leakage and
CC or vascular permeability. The present sequence represents
CC Flt1D2.Flk1D3.FcDELTAC1(a) which is used in an example from the present
CC invention
XX
SQ Sequence 458 AA;

Query Match 98.4%; Score 2399; DB 5; Length 458;
Best Local Similarity 98.7%; Pred. No. 3.9e-151;
Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

```
Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117
```

```
Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        178 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC 237

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
```

RESULT 5
ABP52450
ID ABP52450 standard; protein; 432 AA.
XX
AC ABP52450;
XX
DT 23-OCT-2002 (first entry)
XX
DE Flt1D2.Flk1D3.FcDELTAC1(a) protein sequence.
XX
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW kidney disease; eye disorder; age-related macular degeneration;
KW diabetic retinopathy.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT Disulfide-bond 27. .76
FT Disulfide-bond 121. .182
FT Disulfide-bond 246. .306
FT Disulfide-bond 352. .410
XX
PN WO200260489-A1.
XX
PD 08-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002466.
XX
PR 31-JAN-2001; 2001US-00773877.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Xia Y, Rudge JS, Yancopoulos GD;
XX
DR WPI; 2002-608488/65.
XX
PT Treating psoriasis and enhancing wound healing in humans comprises the
PT administration of a vascular endothelial cell growth factor (VEGF)
PT antagonist.
XX
PS Example 28; Fig 36; 179pp; English.
XX
CC The present invention describes a method for treating psoriasis and
CC enhancing wound healing in a mammal or a human. The method comprises
CC administering a vascular endothelial cell growth factor (VEGF) antagonist
CC to the mammal or human. A VEGF antagonist has antipsoriatic,
CC antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC nephrotropic and ophthalmological activities. The method can be used in
CC treating psoriasis and enhancing wound healing in humans by administering
CC VEGF antagonist. The method is also useful in treating clinical
CC conditions characterised by vascular permeability, oedema or
CC inflammation, such as brain oedema associated with injury, oedema
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC asthma, burns, kidney diseases, or eye disorders such as age-related
CC macular degeneration and diabetic retinopathy. The method may also be
CC used in making the polypeptide to decrease or inhibit plasma leakage and
CC or vascular permeability. The present sequence represents
CC Flt1D2.Flk1D3.FcDELTAC1(a) which is used in an example from the present
CC invention
XX
SQ Sequence 432 AA;

```
  Query Match             93.4%;  Score 2275.5;  DB 5;  Length 432;
  Best Local Similarity   99.3%;  Pred. No. 5.8e-143;
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy         30 GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKG 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKG 60

Qy         90 FIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLN 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLN 120

Qy        150 CTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLY 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLY 180

Qy        210 TCAASSGLMTKKNSTFVRVHEK---DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR 266
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        181 TCAASSGLMTKKNSTFVRVHEKGPGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR 240

Qy        267 TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 300

Qy        327 GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS 360

Qy        387 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH 420

Qy        447 YTQKSLSLSPGK 458
              ||||||||||||
Db        421 YTQKSLSLSPGK 432
```

RESULT 6
AAY97595
ID AAY97595 standard; protein; 455 AA.
XX
AC AAY97595;
XX
DT 05-APR-2001 (first entry)
XX
DE Flt1 receptor fusion protein Flt1D2.VEGFR3D3.FcDeltaC1(a).
XX
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IgG Fc region.
XX
OS Unidentified.
XX
PN WO200075319-A1.
XX

```
PD   14-DEC-2000.
XX
PF   23-MAY-2000; 2000WO-US014142.
XX
PR   08-JUN-1999;   99US-0138133P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Papadopoulos NJ,  Davis S,  Yancopoulos GD;
XX
DR   WPI; 2001-071076/08.
DR   N-PSDB; AAA91075.
XX
PT   Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT   and its fragments, useful for diagnosis, evaluation, and treatment of
PT   diseases associated with the gene expression and for producing model
PT   systems.
XX
PS   Claim 49; Fig 22; 159pp; English.
XX
CC   This sequence represents a fusion protein of the invention between the
CC   Flt1 receptor and the Fc region of IgG. The specification relates to
CC   modified chimeric polypeptides with improved pharmacokinetics. The
CC   modified chimeric polypeptides are preferably Flt1 receptor polypeptides
CC   that have been modified to improve their pharmacokinetic profile. The
CC   polypeptides can be used to decrease or inhibit plasma leakage and/or
CC   vascular permeability in a mammal
XX
SQ   Sequence 455 AA;

  Query Match             84.9%;  Score 2069.5;  DB 4;  Length 455;
  Best Local Similarity   85.7%;  Pred. No. 3e-129;
  Matches  395;  Conservative   16;  Mismatches   41;  Indels    9;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              |||||||||: | |   :|| |||||||||||   | | |: |:|:||  : :  | |
Db        118 HRQTNTIIDIQLLPRKSLELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPER 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
                |: :|:    | |||  |:: | | | | |::|:   : || | |||    ||||||
Db        178 RSQQTHTELS---SILTIHNVSQHDLGSYVCKANNGIQRFRESTEVIVHENGPGDKTHTC 234

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 294

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 354

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 414

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        415 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 455


RESULT 7
ABP52448
ID   ABP52448 standard; protein; 455 AA.
XX
AC   ABP52448;
XX
DT   23-OCT-2002  (first entry)
XX
DE   Modified Flt1 receptor Flt1D2.VEGFR3D3.FcDELTAC1(a) protein sequence.
XX
KW   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW   psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW   vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW   ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW   brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW   kidney disease; eye disorder; age-related macular degeneration;
KW   diabetic retinopathy.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200260489-A1.
XX
PD   08-AUG-2002.
XX
PF   28-JAN-2002; 2002WO-US002466.
XX
PR   31-JAN-2001; 2001US-00773877.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Xia Y,  Rudge JS,  Yancopoulos GD;
XX
DR   WPI; 2002-608488/65.
DR   N-PSDB; ABQ74609.
XX
PT   Treating psoriasis and enhancing wound healing in humans comprises the
PT   administration of a vascular endothelial cell growth factor (VEGF)
PT   antagonist.
XX
PS   Example 17; Fig 22A-C; 179pp; English.
XX
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence represents
CC   Flt1D2.VEGFR3D3.FcDELTAC1(a) which is used in an example from the present
CC   invention
XX
SQ   Sequence 455 AA;

  Query Match             84.9%;  Score 2069.5;  DB 5;  Length 455;
  Best Local Similarity   85.7%;  Pred. No. 3e-129;
  Matches  395;  Conservative   16;  Mismatches   41;  Indels    9;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              |||||||||: | |   :|| |||||||||||   | | |: |:|:||  : :  | |
Db        118 HRQTNTIIDIQLLPRKSLELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPER 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
```

```
                |: :|:    | |||  |:: | | | | |::|:   : || | |||    ||||||
Db        178 RSQQTHTELS---SILTIHNVSQHDLGSYVCKANNGIQRFRESTEVIVHENGPGDKTHTC 234

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 294

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 354

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 414

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        415 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 455
```

RESULT 8
AAY97592
ID AAY97592 standard; protein; 462 AA.
XX
AC AAY97592;
XX
DT 05-APR-2001 (first entry)
XX
DE Flt1 receptor fusion protein Mut3:Flt1(2-3)-Fc.
XX
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IgG Fc region.
XX
OS Unidentified.
XX
PN WO200075319-A1.
XX
PD 14-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US014142.
XX
PR 08-JUN-1999; 99US-0138133P.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Papadopoulos NJ, Davis S, Yancopoulos GD;
XX
DR WPI; 2001-071076/08.
DR N-PSDB; AAA91072.
XX
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model
PT systems.
XX
PS Claim 49; Fig 15; 159pp; English.
XX
CC This sequence represents a fusion protein of the invention between the
CC Flt1 receptor and the Fc region of IgG. The specification relates to
CC modified chimeric polypeptides with improved pharmacokinetics. The
CC modified chimeric polypeptides are preferably Flt1 receptor polypeptides
CC that have been modified to improve their pharmacokinetic profile. The
CC polypeptides can be used to decrease or inhibit plasma leakage and/or
CC vascular permeability in a mammal
XX
SQ Sequence 462 AA;

```
  Query Match             84.1%;  Score 2049;  DB 4;  Length 462;
  Best Local Similarity   84.2%;  Pred. No. 7.1e-128;
  Matches  393;  Conservative   13;  Mismatches   47;  Indels   14;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              |||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
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```
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              |||||||||| :|    ::|  |  ||||||| | ||  :   | ||  |::   : |
Db        118 HRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRR- 176

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK--------- 231
                 | |    | | |||| :   |:|||||   ||   |  :| | :::|
Db        177 -IDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSC 235

Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 295

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 355

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 415

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        416 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462
```

RESULT 9
ABP52445
ID ABP52445 standard; protein; 462 AA.
XX
AC ABP52445;
XX
DT 23-OCT-2002 (first entry)
XX
DE Mutation 3 Flt1(2-3)-Fc protein sequence.
XX
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW kidney disease; eye disorder; age-related macular degeneration;
KW diabetic retinopathy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200260489-A1.
XX
PD 08-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002466.
XX
PR 31-JAN-2001; 2001US-00773877.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Xia Y, Rudge JS, Yancopoulos GD;
XX
DR WPI; 2002-608488/65.
DR N-PSDB; ABQ74606.
XX
PT Treating psoriasis and enhancing wound healing in humans comprises the
PT administration of a vascular endothelial cell growth factor (VEGF)
PT antagonist.
XX
PS Example 13; Fig 15A-C; 179pp; English.
XX

```
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence represents Mut3:Flt1(2-3)
CC   -Fc which is used in an example from the present invention
XX
SQ   Sequence 462 AA;

  Query Match             84.1%;  Score 2049;  DB 5;  Length 462;
  Best Local Similarity   84.2%;  Pred. No. 7.1e-128;
  Matches  393;  Conservative   13;  Mismatches   47;  Indels   14;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              |||||||||| :|    ::|   |  ||||||| | ||  :   | ||  |::   :  |
Db        118 HRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRR- 176

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK--------- 231
                 || |    | | |||| :   |:|||||   ||    |  :| | :::|
Db        177 -IDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSC 235

Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 295

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 355

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 415

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        416 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462


RESULT 10
AAY97591
ID   AAY97591 standard; protein; 452 AA.
XX
AC   AAY97591;
XX
DT   05-APR-2001  (first entry)
XX
DE   Flt1 receptor fusion protein Mut2:Flt1(2-3deltaB)-Fc.
XX
KW   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW   plasma leakage; vascular permeability; IgG Fc region.
XX
OS   Unidentified.
XX
PN   WO200075319-A1.
XX
PD   14-DEC-2000.
XX
PF   23-MAY-2000; 2000WO-US014142.
XX
PR   08-JUN-1999;   99US-0138133P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Papadopoulos NJ,  Davis S,  Yancopoulos GD;
XX
DR   WPI; 2001-071076/08.
DR   N-PSDB; AAA91071.
XX
PT   Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT   and its fragments, useful for diagnosis, evaluation, and treatment of
PT   diseases associated with the gene expression and for producing model
PT   systems.
XX
PS   Claim 49; Fig 14; 159pp; English.
XX
CC   This sequence represents a fusion protein of the invention between the
CC   Flt1 receptor and the Fc region of IgG. The specification relates to
CC   modified chimeric polypeptides with improved pharmacokinetics. The
CC   modified chimeric polypeptides are preferably Flt1 receptor polypeptides
CC   that have been modified to improve their pharmacokinetic profile. The
CC   polypeptides can be used to decrease or inhibit plasma leakage and/or
CC   vascular permeability in a mammal
XX
SQ   Sequence 452 AA;

  Query Match             83.6%;  Score 2038;  DB 4;  Length 452;
  Best Local Similarity   83.9%;  Pred. No. 3.7e-127;
  Matches  392;  Conservative   10;  Mismatches   41;  Indels   24;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              |||||||||| :|    ::|   |  ||||||| | ||  :   | ||             |
Db        118 HRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYP-----------D 165

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK--------- 231
                 || |    | | |||| :   |:|||||   ||    |  :| | :::|
Db        166 EIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSC 225

Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 285

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 345

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 405

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        406 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 11
ABP52444
ID   ABP52444 standard; protein; 452 AA.
XX
AC   ABP52444;
XX
```

```
DT   23-OCT-2002  (first entry)
XX
DE   Mutation 2 Flt1(2-3 delta B)-Fc protein sequence.
XX
KW   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW   psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW   vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW   ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW   brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW   kidney disease; eye disorder; age-related macular degeneration;
KW   diabetic retinopathy.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200260489-A1.
XX
PD   08-AUG-2002.
XX
PF   28-JAN-2002; 2002WO-US002466.
XX
PR   31-JAN-2001; 2001US-00773877.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Xia Y,  Rudge JS,  Yancopoulos GD;
XX
DR   WPI; 2002-608488/65.
DR   N-PSDB; ABQ74605.
XX
PT   Treating psoriasis and enhancing wound healing in humans comprises the
PT   administration of a vascular endothelial cell growth factor (VEGF)
PT   antagonist.
XX
PS   Example 12; Fig 14A-C; 179pp; English.
XX
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
CC   or vascular permeability. The present sequence represents Mut2:Flt1(2-3
CC   delta B)-Fc which is used in an example from the present invention
XX
SQ   Sequence 452 AA;

  Query Match             83.6%;  Score 2038;  DB 5;  Length 452;
  Best Local Similarity   83.9%;  Pred. No. 3.7e-127;
  Matches  392;  Conservative   10;  Mismatches   41;  Indels   24;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              |||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              |||||||||| :|    ::|  |  ||||||| | ||  :   | ||            |
Db        118 HRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYP----------D 165

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK--------- 231
                 || |    | | |||| :   |:|||||   ||   |  :| | :::|
```

```
Db        166 EIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSC 225

Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 285

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 345

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 405

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        406 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
```

```
RESULT 12
AAY97593
ID   AAY97593 standard; protein; 567 AA.
XX
AC   AAY97593;
XX
DT   05-APR-2001  (first entry)
XX
DE   Flt1 receptor fusion protein Mut4:Flt1(1-3R-N)-Fc.
XX
KW   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW   plasma leakage; vascular permeability; IgG Fc region.
XX
OS   Unidentified.
XX
PN   WO200075319-A1.
XX
PD   14-DEC-2000.
XX
PF   23-MAY-2000; 2000WO-US014142.
XX
PR   08-JUN-1999;   99US-0138133P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Papadopoulos NJ,  Davis S,  Yancopoulos GD;
XX
DR   WPI; 2001-071076/08.
DR   N-PSDB; AAA91073.
XX
PT   Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT   and its fragments, useful for diagnosis, evaluation, and treatment of
PT   diseases associated with the gene expression and for producing model
PT   systems.
XX
PS   Claim 49; Fig 16; 159pp; English.
XX
CC   This sequence represents a fusion protein of the invention between the
CC   Flt1 receptor and the Fc region of IgG. The specification relates to
CC   modified chimeric polypeptides with improved pharmacokinetics. The
CC   modified chimeric polypeptides are preferably Flt1 receptor polypeptides
CC   that have been modified to improve their pharmacokinetic profile. The
CC   polypeptides can be used to decrease or inhibit plasma leakage and/or
CC   vascular permeability in a mammal
XX
SQ   Sequence 567 AA;

  Query Match             82.7%;  Score 2015.5;  DB 4;  Length 567;
  Best Local Similarity   69.6%;  Pred. No. 1.5e-125;
  Matches  396;  Conservative   14;  Mismatches   46;  Indels  113;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSG---------------------------------- 26
              |||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK 60
```

```
Qy          27 ------------------------------------------------------------ 26

Db          61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET 120

Qy          27 --------SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 78
                     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 180

Qy          79 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI 138
               ||||||||||||||||||||||||||||||||||||||||||||||||||||| :|    :
Db         181 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV 240

Qy         139 ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
               :|  |  ||||||| | ||  :   | ||  |::: : |    || |    | | |||
Db         241 KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKNASVRRR--IDQSNSHANIFYSVLTI 298

Qy         199 DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---------DKTHTCPPCPAPELLGGP 249
               | :   |:|||||   ||   |  :| | :::|         ||||||||||||||||
Db         299 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 358

Qy         250 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418

Qy         310 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 478

Qy         370 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538

Qy         430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
               ||||||||||||||||||||||||||||
Db         539 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567
```

RESULT 13
ABP52446
ID ABP52446 standard; protein; 567 AA.
XX
AC ABP52446;
XX
DT 23-OCT-2002 (first entry)
XX
DE Mutation 4 Flt1(2-3 R->N)-Fc protein sequence.
XX
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW kidney disease; eye disorder; age-related macular degeneration;
KW diabetic retinopathy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200260489-A1.
XX
PD 08-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002466.
XX
PR 31-JAN-2001; 2001US-00773877.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Xia Y, Rudge JS, Yancopoulos GD;
XX
DR WPI; 2002-608488/65.
DR N-PSDB; ABQ74607.
XX
PT Treating psoriasis and enhancing wound healing in humans comprises the
PT administration of a vascular endothelial cell growth factor (VEGF)
PT antagonist.
XX
PS Example 14; Fig 16A-D; 179pp; English.
XX
CC The present invention describes a method for treating psoriasis and
CC enhancing wound healing in a mammal or a human. The method comprises
CC administering a vascular endothelial cell growth factor (VEGF) antagonist
CC to the mammal or human. A VEGF antagonist has antipsoriatic,
CC antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC nephrotropic and ophthalmological activities. The method can be used in
CC treating psoriasis and enhancing wound healing in humans by administering
CC VEGF antagonist. The method is also useful in treating clinical
CC conditions characterised by vascular permeability, oedema or
CC inflammation, such as brain oedema associated with injury, oedema
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC asthma, burns, kidney diseases, or eye disorders such as age-related
CC macular degeneration and diabetic retinopathy. The method may also be
CC used in making the polypeptide to decrease or inhibit plasma leakage and
CC or vascular permeability. The present sequence represents Mut4:Flt1(2-3 R
CC ->N)-Fc which is used in an example from the present invention
XX
SQ Sequence 567 AA;

Query Match 82.7%; Score 2015.5; DB 5; Length 567;
Best Local Similarity 69.6%; Pred. No. 1.5e-125;
Matches 396; Conservative 14; Mismatches 46; Indels 113; Gaps 3;

```
Qy           1 MVSYWDTGVLLCALLSCLLLTGSSSG---------------------------------- 26
                 ||||||||||||||||||||||||||
Db           1 MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK 60

Qy          27 ------------------------------------------------------------ 26

Db          61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET 120

Qy          27 --------SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 78
                     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 180

Qy          79 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI 138
               ||||||||||||||||||||||||||||||||||||||||||||||||||||| :|    :
Db         181 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV 240

Qy         139 ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
               :|  |  ||||||| | ||  :   | ||  |::: : |    || |    | | |||
Db         241 KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKNASVRRR--IDQSNSHANIFYSVLTI 298

Qy         199 DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---------DKTHTCPPCPAPELLGGP 249
               | :   |:|||||   ||   |  :| | :::|         ||||||||||||||||
Db         299 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 358

Qy         250 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418

Qy         310 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 478

Qy         370 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538

Qy         430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
               ||||||||||||||||||||||||||||
Db         539 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567
```

RESULT 14
AAY97597

```
ID   AAY97597 standard; protein; 567 AA.
XX
AC   AAY97597;
XX
DT   05-APR-2001  (first entry)
XX
DE   Flt1 receptor fusion protein Flt1(1-3)-Fc.
XX
KW   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW   plasma leakage; vascular permeability; IgG Fc region.
XX
OS   Unidentified.
XX
PN   WO200075319-A1.
XX
PD   14-DEC-2000.
XX
PF   23-MAY-2000; 2000WO-US014142.
XX
PR   08-JUN-1999;   99US-0138133P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Papadopoulos NJ,  Davis S,  Yancopoulos GD;
XX
DR   WPI; 2001-071076/08.
DR   N-PSDB; AAA91077.
XX
PT   Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT   and its fragments, useful for diagnosis, evaluation, and treatment of
PT   diseases associated with the gene expression and for producing model
PT   systems.
XX
PS   Example 11; Fig 10; 159pp; English.
XX
CC   This sequence represents a fusion protein of the invention between the
CC   Flt1 receptor and the Fc region of IgG. The specification relates to
CC   modified chimeric polypeptides with improved pharmacokinetics. The
CC   modified chimeric polypeptides are preferably Flt1 receptor polypeptides
CC   that have been modified to improve their pharmacokinetic profile. The
CC   polypeptides can be used to decrease or inhibit plasma leakage and/or
CC   vascular permeability in a mammal
XX
SQ   Sequence 567 AA;

  Query Match             82.7%;  Score 2014.5;  DB 4;  Length 567;
  Best Local Similarity   69.6%;  Pred. No. 1.8e-125;
  Matches  396;  Conservative   13;  Mismatches   47;  Indels  113;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSG---------------------------------- 26
              |||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK 60

Qy         27 ------------------------------------------------------------ 26

Db         61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET 120

Qy         27 --------SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 78
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 180

Qy         79 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI 138
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| :|    :
Db        181 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV 240

Qy        139 ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
              :|  |  ||||||| | ||  :   | ||  |::  :  |    || |    | | |||
Db        241 KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRR--IDQSNSHANIFYSVLTI 298

Qy        199 DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---------DKTHTCPPCPAPELLGGP 249
              | :   |:|||||   ||   |  :| | :::|         ||||||||||||||||
Db        299 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 358

Qy        250 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418

Qy        310 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 478

Qy        370 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538

Qy        430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||
Db        539 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567


RESULT 15
ABP52442
ID   ABP52442 standard; protein; 567 AA.
XX
AC   ABP52442;
XX
DT   23-OCT-2002  (first entry)
XX
DE   Flt1(1-3)-Fc protein sequence.
XX
KW   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW   psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
KW   vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW   ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW   brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW   kidney disease; eye disorder; age-related macular degeneration;
KW   diabetic retinopathy.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200260489-A1.
XX
PD   08-AUG-2002.
XX
PF   28-JAN-2002; 2002WO-US002466.
XX
PR   31-JAN-2001; 2001US-00773877.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Xia Y,  Rudge JS,  Yancopoulos GD;
XX
DR   WPI; 2002-608488/65.
DR   N-PSDB; ABQ74603.
XX
PT   Treating psoriasis and enhancing wound healing in humans comprises the
PT   administration of a vascular endothelial cell growth factor (VEGF)
PT   antagonist.
XX
PS   Example 11; Fig 10A-D; 179pp; English.
XX
CC   The present invention describes a method for treating psoriasis and
CC   enhancing wound healing in a mammal or a human. The method comprises
CC   administering a vascular endothelial cell growth factor (VEGF) antagonist
CC   to the mammal or human. A VEGF antagonist has antipsoriatic,
CC   antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,
CC   nephrotropic and ophthalmological activities. The method can be used in
CC   treating psoriasis and enhancing wound healing in humans by administering
CC   VEGF antagonist. The method is also useful in treating clinical
CC   conditions characterised by vascular permeability, oedema or
CC   inflammation, such as brain oedema associated with injury, oedema
CC   associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC   asthma, burns, kidney diseases, or eye disorders such as age-related
CC   macular degeneration and diabetic retinopathy. The method may also be
CC   used in making the polypeptide to decrease or inhibit plasma leakage and
```

```
CC   or vascular permeability. The present sequence represents Flt1(1-3)-Fc
CC   which is used in an example from the present invention
XX
SQ   Sequence 567 AA;

  Query Match           82.7%;  Score 2014.5;  DB 5;  Length 567;
  Best Local Similarity 69.6%;  Pred. No. 1.8e-125;
  Matches  396;  Conservative   13;  Mismatches   47;  Indels  113;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSG---------------------------------- 26
              |||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK 60

Qy         27 ------------------------------------------------------------ 26

Db         61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET 120

Qy         27 --------SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 78
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 180

Qy         79 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI 138
              |||||||||||||||||||||||||||||||||||||||||||||||||| :|    :
Db        181 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV 240

Qy        139 ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
              :|  |  ||||||| | ||  :   | ||  |::   :  |    || |    | | |||
Db        241 KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRR--IDQSNSHANIFYSVLTI 298

Qy        199 DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---------DKTHTCPPCPAPELLGGP 249
              | :   |:|||||   ||   |  :| | :::|         ||||||||||||||||
Db        299 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 358

Qy        250 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418

Qy        310 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 478

Qy        370 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538

Qy        430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||
Db        539 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567


Search completed: September 23, 2005, 17:14:53
Job time : 125 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 23, 2005, 16:52:28 ; Search time 39 Seconds
(without alignments)
1129.930 Million cell updates/sec

Title: US-10-811-170-2
Perfect score: 2437
Sequence: 1 MVSYWDTGVLLCALLSCLLL.....MHEALHNHYTQKSLSLSPGK 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1240.5	50.9	330	1	GHHU	Ig gamma-1 chain C
2	1240.5	50.9	374	2	S69339	Ig heavy chain V r
3	1233	50.6	255	4	S31866	Ig gamma-1 chain C
4	1180	48.4	234	2	PT0207	Ig gamma chain C r
5	1148.5	47.1	326	1	G2HU	Ig gamma-2 chain C
6	1146	47.0	377	2	A23511	Ig gamma-3 chain C
7	1144	46.9	327	1	G4HU	Ig gamma-4 chain C
8	1144	46.9	377	2	A60764	Ig gamma-3 chain C
9	1121	46.0	289	1	G3HUWI	Ig gamma-3 heavy c
10	929.5	38.1	328	2	I47160	Ig gamma 2b chain
11	929.5	38.1	328	2	I47159	Ig gamma 2a chain
12	925.5	38.0	323	1	GHRB	Ig gamma chain C r
13	917.5	37.6	277	2	I47162	Ig gamma 4 chain c
14	913.5	37.5	328	2	I47158	Ig gamma 1 chain c
15	900	36.9	329	1	G2GP	Ig gamma-2 chain C
16	899.5	36.9	328	2	I47161	Ig gamma 3 chain c
17	870	35.7	470	2	S22080	Ig heavy chain pre
18	866.5	35.6	329	1	G3MSC	Ig gamma-3 chain C
19	863.5	35.4	472	2	S31459	Ig gamma-1 chain -
20	855.5	35.1	398	1	G3MSM	Ig gamma-3 chain C
21	854.5	35.1	444	2	PC4436	monoclonal antibod
22	852	35.0	308	2	C30554	Ig heavy chain C r
23	844	34.6	333	2	PS0018	Ig gamma-2b chain
24	843.5	34.6	469	2	S37483	Ig gamma-2a chain
25	837.5	34.4	330	1	G2MSA	Ig gamma-2a chain
26	833.5	34.2	324	1	G1MS	Ig gamma-1 chain C
27	832.5	34.2	399	1	G2MSAM	Ig gamma-2a chain
28	832	34.1	329	2	S00847	Ig gamma-2c chain
29	831.5	34.1	326	2	PS0017	Ig gamma-1 chain C
30	828.5	34.0	393	1	G1MSM	Ig gamma-1 chain C
31	827	33.9	446	2	S40295	Ig gamma-2a chain
32	825	33.9	335	1	G2MSAB	Ig gamma-2a chain
33	809	33.2	474	1	G2MS11	Ig gamma-2b chain
34	807.5	33.1	322	2	PS0019	Ig gamma-2a chain
35	803.5	33.0	405	1	G2MSBM	Ig gamma-2b chain
36	801.5	32.9	687	2	A49636	soluble vascular e
37	801.5	32.9	1338	2	S09982	protein-tyrosine k
38	793	32.5	475	2	S01321	Ig gamma-2b chain
39	771.5	31.7	327	2	S06611	Ig gamma-2 chain C
40	724	29.7	1356	2	JC1402	protein-tyrosine k
41	707	29.0	180	2	I46732	Ig gamma heavy cha
42	700.5	28.7	1336	2	I60598	Fit-1 tyrosine kin
43	679	27.9	1333	2	I78875	receptor tyrosine
44	653.5	26.8	1330	2	S49010	embryonic receptor
45	582.5	23.9	218	2	A36040	Ig heavy chain V-I

ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 50.9%; Score 1240.5; DB 1; Length 330;
Best Local Similarity 86.4%; Pred. No. 1.3e-71;
Matches 242; Conservative 7; Mismatches 12; Indels 19; Gaps 5;

```
Qy        197 TIDGVTRSDQGLYTCAA-----SSGLMT---------KKNSTFV--RVHEK--DKTHTCP 238
              |   | :|  |||: ::     || | |          | ::| |  :|  |  |||||||
Db         52 TFPAVLQS-SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP 110

Qy        239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 170

Qy        299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 230

Qy        359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 290

Qy        419 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        291 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 2
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 50.9%; Score 1240.5; DB 2; Length 374;
Best Local Similarity 72.9%; Pred. No. 1.5e-71;
Matches 248; Conservative 17; Mismatches 50; Indels 25; Gaps 6;

```
Qy        144 EKLVLNCT----ARTELNVGIDFNWEYPSSKHQHKKLVNRD--------LKTQ--SGSEM 189
              : | | ||    : ::  ||: :  : |    :   |: |         |:|:    :
Db         35 QTLTLTCTFSGFSLSKSGVGVGWIRQPPGQALEWLALIFWDDDKRYSPSLRTRLTITKDT 94

Qy        190 KKFLSTLTIDGVTRSDQGLYTCAAS-----SGLMTKK--NSTFVRVHEK----DKTHTCP 238
               |    ||:  |  :|   | | |       |          | | |  :    |||||||
Db         95 SKNQVVLTMTNVDPADTATYYCGYSVEGYGQGYRFHSWGQGTLVTVSSEPKSCDKTHTCP 154

Qy        239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 214

Qy        299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 274

Qy        359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 418
              ||||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 334

Qy        419 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        335 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374
```

RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 50.6%; Score 1233; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 2.9e-71;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 88

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 208

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        209 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255
```

RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 48.4%; Score 1180; DB 2; Length 234;
Best Local Similarity 98.6%; Pred. No. 6e-68;
Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              | |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 DTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTPPVLDS 194

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 451
              |||||||||||||||||||||||||||||||||||||||||
Db        195 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 234
```

RESULT 5
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a h
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-2
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin ga
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.1%; Score 1148.5; DB 1; Length 326;
Best Local Similarity 80.0%; Pred. No. 9e-66;
Matches 224; Conservative 13; Mismatches 20; Indels 23; Gaps 6;

```
Qy        197 TIDGVTRSDQGLYTCAASSGLMTKKNSTF------VRVHEK------DKT------HTCP 238
              |   | :|  |||:    | ::|  :| |       |  |      |||       ||
Db         52 TFPAVLQS-SGLYSL---SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECP 107

Qy        239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298
              |||||  : |||||||||||||||||||||||||||||||||||:||||||||||||
Db        108 PCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNA 166

Qy        299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358
              ||||||||:|||:||||||||:|||||||||||||||| |||||||||| ||||||||
Db        167 KTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQ 226

Qy        359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 418
              ||||||||:|:|||||||||||||||||||||||||||||||||||:||||||||||
```

```
Db        227 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLY 286

Qy        419 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        287 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326


RESULT 6
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: co
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             47.0%;  Score 1146;  DB 2;  Length 377;
  Best Local Similarity   92.5%;  Pred. No. 1.5e-65;
  Matches  210;  Conservative    8;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              |    || |||||||||||||||||||||||||||||||||||||||||||||||:| ||||
Db        151 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 210

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||| |
Db        211 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              |||||||||||||||:|:|||||||||||||||||||||:||||||| ||||:|||
Db        271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 330

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              ||||||||||||||||||||:||||||||||| :||||||||||
Db        331 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK 377


RESULT 7
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             46.9%;  Score 1144;  DB 1;  Length 327;
  Best Local Similarity   79.9%;  Pred. No. 1.7e-65;
  Matches  222;  Conservative   14;  Mismatches   24;  Indels   18;  Gaps    4;

Qy        197 TIDGVTRSDQGLYTCAA-----SSGLMTKKNSTFVRVHEKDKTHT-----------CPPC 240
              |   | :|  |||: ::     || | ||  :  |  |:   |              || |
Db         52 TFPAVLQS-SGLYSLSSVVTVPSSSLGTKTYTCNVD-HKPSNTKVDKRVESKYGPPCPSC 109

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              |||| ||||||||||||||||||||||||||||||| |||||:|||||||||||||||
Db        110 PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT 169

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||:|||||||||||||||||||||||||||| ||: ||||||||||||||||||
Db        170 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVY 229

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              |||||::|:|||||||||||||||||||||||||||||||||||||||||||||||||:
Db        230 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR 289

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||:|||||||||||||||||||||| ||
Db        290 LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 8
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 converte
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             46.9%;  Score 1144;  DB 2;  Length 377;
  Best Local Similarity   92.5%;  Pred. No. 2.1e-65;
  Matches  210;  Conservative    8;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              |    || |||||||||||||||||||||||||||||||||||||||||||||:| ||||
Db        151 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 210

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||| |
Db        211 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
```

```
Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              |||||||||||||||:|:|||||||||||||||||||||||:|||||| ||||||||
Db        271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPVLDS 330

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              ||||||||:|||||||||:|||||||||||||| :||||||||||
Db        331 DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNRFTQKSLSLSPGK 377


RESULT 9
G3HUWI
Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-
A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Molecule type: protein
A;Residues: 1-289 <FRA>
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A;Accession: A90198
A;Molecule type: protein
A;Residues: 59-125,'EB',128-226,228-289 <WOL>
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             46.0%;  Score 1121;  DB 1;  Length 289;
  Best Local Similarity   90.3%;  Pred. No. 4.3e-64;
  Matches  204;  Conservative   13;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              |   || |||||||||||||||||||||||||||||||||||||||||||:| ||||
Db         64 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 123

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||:||||||||||:|:|||:||||||||||:||:|||||||||||||||||||||| |
Db        124 GVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              |||||||||||||:|:|||||||||||||||||||||||:||||||| ||||:|||
Db        184 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 243

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 457
              ||||||||||||||||||:||||||||||| :||||||||||
Db        244 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG 289


RESULT 10
I47160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             38.1%;  Score 929.5;  DB 2;  Length 328;
  Best Local Similarity   56.1%;  Pred. No. 7.2e-52;
  Matches  180;  Conservative   41;  Mismatches   83;  Indels   17;  Gaps    5;

Qy        143 GEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTID 199
              |  : | | | :     :   |       |  |    ::         | :    | :|:
Db         20 GPNVALGCLASSYFPEPVTVTWNSGALTSGVHTFPSVL-------QPSGLYSLSSMVTVP 72

Qy        200 GVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPK 259
                : | :  |||  :    | |    |    |     || | :|    |||||:||||||
Db         73 ASSLSSKS-YTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----GPSVFIFPPKPK 127

Qy        260 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 319
              |||||||||:|||||||||| |:|||:|:|||||||| |:|:|:|||:|||||||||| :
Db        128 DTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPI 187

Qy        320 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 379
              |||||||||:||||:|| ||||| : ||||||| ||||||||||  :||:::::||:|||
Db        188 QHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEELSRSKVSITCL 247

Qy        380 VKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 437
              | |||| || |||: |||  || ||:||||  | ||::||||| :|||: || | :| |:
Db        248 VIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKASWQQGGQIFQCA 307

Qy        438 VMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||:| :|||
Db        308 VMHEALHNHYTQKSISKTPGK 328


RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
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A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match            38.1%;  Score 929.5;  DB 2;  Length 328;
  Best Local Similarity  56.1%;  Pred. No. 7.2e-52;
  Matches  180;  Conservative   41;  Mismatches   83;  Indels   17;  Gaps    5;

Qy        143 GEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTID 199
              |  : | | | :    :   |     |  |    ::         | :    | :|:
Db         20 GPNVALGCLASSYFPEPVTVTWNSGALSSGVHTFPSVL-------QPSGLYSLSSMVTVP 72

Qy        200 GVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPK 259
                : | :  |||  :    | |    |     |      || | :|    |||||:||||||
Db         73 ASSLSSKS-YTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----GPSVFIFPPKPK 127

Qy        260 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 319
              |||||||||:|||||||| |:|||:|:|||||||| |:|:|:|||:|||||||||| :
Db        128 DTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPI 187

Qy        320 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 379
              |||||||||:||||:|| ||||| : ||||||| ||||||||| :||::::||:|||
Db        188 QHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEELSRSKVSITCL 247

Qy        380 VKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 437
              | |||| || |||: |||  || ||:|||| | ||::|||||  :|||: || | :| |:
Db        248 VIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKASWQGGGIFQCA 307

Qy        438 VMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||:| :|||
Db        308 VMHEALHNHYTQKSISKTPGK 328


RESULT 12
GHRB
Ig gamma chain C region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot
A;Reference number: A91749; MUID:84030930; PMID:6313520
A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
A;Cross-references: UNIPROT:P01870
A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R;Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A;Reference number: A90290; MUID:76135469; PMID:1243651
A;Accession: A90290
A;Molecule type: protein
A;Residues: 1-47,'E',49-71,'PV',72-128 <PRA>
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A;Reference number: A93928; MUID:83299917; PMID:6193512
A;Accession: A93928
A;Molecule type: mRNA
A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A;Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marke
R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C
A;Reference number: A90245; MUID:70110015; PMID:5461106
A;Accession: A90245
A;Molecule type: protein
A;Residues: 132-143,'E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A;Reference number: A94416
A;Accession: A94416
A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',2
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            38.0%;  Score 925.5;  DB 1;  Length 323;
  Best Local Similarity  64.3%;  Pred. No. 1.3e-51;
  Matches  180;  Conservative   33;  Mismatches   50;  Indels   17;  Gaps    6;

Qy        195 TLTIDGV-----TRSDQGLYTCAA-----SSGLMTKKNSTFVRVHEK-DKT---HTC--P 238
              ||| :||      |   |||: ::     ||       |      : | |||    ||  |
Db         45 TLT-NGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKP 103

Qy        239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298
              || |||||||||:|||||||||||||||||||||||| :||||:| ||::  :|  |
Db        104 TCPPPELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTA 163

Qy        299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358
              :   ||:|:||| |||| | : ||||| |||:|||| ||||||||||||||:||| ||:
Db        164 RPPLREQQFNSTIRVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPK 223

Qy        359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 418
              |||: | |:||:   |||||:: |||||||:|||| ||: |:|||||| |||||||:|||
Db        224 VYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLY 283

Qy        419 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              :||:|  | ||:|:||:|||||||||||||||:| ||||
Db        284 NKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK 323


RESULT 13
I47162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a si
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>

  Query Match            37.6%;  Score 917.5;  DB 2;  Length 277;
  Best Local Similarity  64.7%;  Pred. No. 3.4e-51;
  Matches  174;  Conservative   36;  Mismatches   48;  Indels   11;  Gaps    5;

Qy        194 STLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPCP-APELLG-GPSV 251
              | :|:   : | :  |||  :    | |      | ::  | | ||||  |   | |||
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```
Db         16 SMVTVPASSLSSKS-YTCNVNHPATTTK------VDKRVGTKTKPPCPICPACEGPGPSA 68

Qy        252 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 311
              |:|||||||||||||:||||||||| |:|||:|:||||||||| |:|:|:|||:|||| 
Db         69 FIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFNSTY 128

Qy        312 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 371
              |||||| : |||||||||:||||:|| ||||| : ||||||| |||||||||| :||:: 
Db        129 RVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPPTEELSR 188

Qy        372 NQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
              ::|:||||| |||| || |||: |||  || ||:|||| | ||::|||||| |||: || 
Db        189 SKVTLTCLVTGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKLAVDKASWQ 248

Qy        430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              :|: | |:|||||||||||||||:  :||| 
Db        249 RGDTFQCAVMHEALHNHYTQKSIFKTPGK 277


RESULT 14
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             37.5%;  Score 913.5;  DB 2;  Length 328;
  Best Local Similarity   56.4%;  Pred. No. 7.4e-51;
  Matches  181;  Conservative   40;  Mismatches   83;  Indels   17;  Gaps    6;

Qy        143 GEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTID 199
              |  : | | | :    :   |      | |    ::        | :    | :|: 
Db         20 GPNVALGCLASSYFPEPVTVTWNSGALTSGVHTFPSVL-------QPSGLYSLSSMVTVP 72

Qy        200 GVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPK 259
                : | :  |||  :    | |    | :|:     ||| ||  | : |||||:|||||| 
Db         73 ASSLSSKS-YTCNVNHPATTTKVDKRVGIHQ---PQTCPICPGCE-VAGPSVFIFPPKPK 127

Qy        260 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 319
              ||||||:|||||||||||| |  ||:|:|||||||| |:|:|:|||:|||||||||| : 
Db        128 DTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEVHTAETRPKEEQFNSTYRVVSVLPI 187

Qy        320 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 379
              ||||| |||:||||:|  ||||| :||||| || |||||||||  :||::::|:|||| 
Db        188 QHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEELSRSKVTLTCL 247

Qy        380 VKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 437
              | |||| || |||:|||| |||| |:|||  | ||:|||||| |||:||  |: | |: 
Db        248 VIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDGTFFLYSKLAVDKARWDHGDKFECA 307

Qy        438 VMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||:| : || 
Db        308 VMHEALHNHYTQKSISKTQGK 328


RESULT 15
G2GP
Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
A;Accession: A94553
A;Molecule type: protein
A;Residues: 1-3 <TRI>
A;Cross-references: UNIPROT:P01862
R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
A;Molecule type: protein
A;Residues: 4-68 <BIR>
R;Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amir
A;Reference number: A90359; MUID:71058486; PMID:5538616
A;Accession: A90359
A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
A;Molecule type: protein
A;Residues: 134-226 <TRA>
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
A;Molecule type: protein
A;Residues: 227-311 <TR2>
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;21-81/Domain: immunoglobulin homology <IM1>
F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental

  Query Match             36.9%;  Score 900;  DB 1;  Length 329;
  Best Local Similarity   55.7%;  Pred. No. 5.4e-50;
  Matches  180;  Conservative   38;  Mismatches   83;  Indels   22;  Gaps    8;

Qy        143 GEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTID 199
              |  : | |  :      :   |      | |    ::       |||  :    | :|: 
Db         21 GSMMTLGCLVKGYFPEPVTVKWNSGALTSGVHTFPAVL------QSG--LYSLTSMVTVP 72

Qy        200 GVTRSDQGLYTC-AASSGLMTKKNSTF--VRVHEKDKTHTCPPCPAPELLGGPSVFLFPP 256
                  ::     ||  |      || : |   :|  : :   ||| || || |||||||:||| 
Db         73 SSQKA-----TCNVAHPASSTKVDKTVEPIRTPZPBPC-TCPKCPPPENLGGPSVFIFPP 126

Qy        257 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV 316
              ||||||||| || ||||||||| ::|||:| |:||   | ||:|||| ||||:|:|| || 
Db        127 KPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKPRVEQYNTTFRVESV 186

Qy        317 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL 376
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            | : ||||| |||:|||| |||||||||||||| || || | ||||||||||:|::||:
Db        187 LPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPSRDELSKSKVSV 246

Qy        377 TCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 434
            |||:  |:|:|| ||| ||  |  |  || |||: |:|||:|||||||||| | || |:
Db        247 TCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSKLTVDKSAWDQGTVY 306

Qy        435 SCSVMHEALHNHYTQKSLSLSPG 457
            :|||||||||| |||::| |||
Db        307 TCSVMHEALHNHVTQKAISRSPG 329


Search completed: September 23, 2005, 17:17:53
Job time : 41 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 23, 2005, 16:57:02 ; Search time 45 Seconds
(without alignments)
759.762 Million cell updates/sec

Title: US-10-811-170-2
Perfect score: 2437
Sequence: 1 MVSYWDTGVLLCALLSCLLL.....MHEALHNHYTQKSLSLSPGK 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2437	100.0	458	4	US-09-773-877B-26	Sequence 26, Appl
2	2399	98.4	458	4	US-09-773-877B-22	Sequence 22, Appl
3	2261	92.8	431	4	US-09-773-877B-27	Sequence 27, Appl
4	2069.5	84.9	455	4	US-09-773-877B-24	Sequence 24, Appl
5	2049	84.1	462	4	US-09-773-877B-18	Sequence 18, Appl
6	2038	83.6	452	4	US-09-773-877B-16	Sequence 16, Appl
7	2015.5	82.7	567	4	US-09-773-877B-20	Sequence 20, Appl
8	2014.5	82.7	567	4	US-09-773-877B-12	Sequence 12, Appl
9	2003.5	82.2	557	4	US-09-773-877B-14	Sequence 14, Appl
10	1304	53.5	680	3	US-08-227-496C-15	Sequence 15, Appl
11	1280	52.5	497	4	US-09-499-846-6	Sequence 6, Appli
12	1279.5	52.5	622	4	US-09-499-846-2	Sequence 2, Appli
13	1275.5	52.3	910	4	US-09-313-942-28	Sequence 28, Appl
14	1274.5	52.3	525	4	US-09-499-846-4	Sequence 4, Appli
15	1269.5	52.1	488	4	US-09-499-846-12	Sequence 12, Appl
16	1269	52.1	388	3	US-09-131-247-16	Sequence 16, Appl
17	1269	52.1	388	4	US-09-784-623-16	Sequence 16, Appl
18	1265	51.9	347	1	US-07-940-861-43	Sequence 43, Appl
19	1265	51.9	347	1	US-08-459-512-43	Sequence 43, Appl
20	1265	51.9	347	2	US-08-459-657-43	Sequence 43, Appl
21	1265	51.9	347	2	US-08-460-132-43	Sequence 43, Appl
22	1265	51.9	347	3	US-08-466-465-8	Sequence 8, Appli
23	1265	51.9	347	4	US-09-730-465-8	Sequence 8, Appli
24	1265	51.9	347	5	PCT-US92-02050-43	Sequence 43, Appl
25	1265	51.9	497	4	US-09-499-846-10	Sequence 10, Appl
26	1261	51.7	459	1	US-08-157-101A-7	Sequence 7, Appli
27	1259.5	51.7	525	4	US-09-499-846-8	Sequence 8, Appli
28	1256	51.5	475	4	US-09-740-002-25	Sequence 25, Appl
29	1254.5	51.5	547	4	US-09-746-359A-54	Sequence 54, Appl
30	1254.5	51.5	571	4	US-09-746-359A-53	Sequence 53, Appl
31	1254.5	51.5	691	4	US-09-313-942-20	Sequence 20, Appl
32	1254.5	51.5	694	4	US-09-313-942-22	Sequence 22, Appl
33	1253.5	51.4	387	1	US-08-470-299-4	Sequence 4, Appli
34	1253.5	51.4	437	5	PCT-US96-10043-11	Sequence 11, Appl
35	1253.5	51.4	704	4	US-09-590-656-2	Sequence 2, Appli
36	1253.5	51.4	704	4	US-09-733-764-2	Sequence 2, Appli
37	1252.5	51.4	450	4	US-09-996-288-248	Sequence 248, App
38	1252.5	51.4	467	4	US-08-030-175-42	Sequence 42, Appl
39	1251.5	51.4	450	4	US-09-996-288-210	Sequence 210, App
40	1251.5	51.4	450	4	US-09-996-288-222	Sequence 222, App
41	1251.5	51.4	450	4	US-09-996-288-224	Sequence 224, App
42	1251.5	51.4	450	4	US-09-996-288-228	Sequence 228, App
43	1251.5	51.4	450	4	US-09-996-288-238	Sequence 238, App
44	1251.5	51.4	450	4	US-09-996-288-240	Sequence 240, App
45	1251.5	51.4	450	4	US-09-996-288-242	Sequence 242, App

ALIGNMENTS

RESULT 1
US-09-773-877B-26
; Sequence 26, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VEGFR1R2-FcdeltaC1(a) Receptor
US-09-773-877B-26

Query Match 100.0%; Score 2437; DB 4; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.3e-196;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 2
US-09-773-877B-22
; Sequence 22, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1D2.Flk1D3.FcdeltaC1(a) Receptor
US-09-773-877B-22

  Query Match             98.4%;  Score 2399;  DB 4;  Length 458;
  Best Local Similarity   98.7%;  Pred. No. 2e-193;
  Matches  455;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    2;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
              |||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        178 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC 237

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 3
US-09-773-877B-27
; Sequence 27, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide
US-09-773-877B-27

  Query Match             92.8%;  Score 2261;  DB 4;  Length 431;
  Best Local Similarity   99.1%;  Pred. No. 7.5e-182;
  Matches  428;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    2;

Qy         30 GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKG 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKG 60

Qy         90 FIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLN 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLN 120

Qy        150 CTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLY 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLY 180

Qy        210 TCAASSGLMTKKNSTFVRVHEK---DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR 266
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        181 TCAASSGLMTKKNSTFVRVHEKGPGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR 240

Qy        267 TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 300

Qy        327 GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS 386
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        301 GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS-TCLVKGFYPS 359

Qy        387 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH 419

Qy        447 YTQKSLSLSPGK 458
              ||||||||||||
Db        420 YTQKSLSLSPGK 431


RESULT 4
US-09-773-877B-24
; Sequence 24, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1D2.VEGFR3D3.FcdeltaC1(a)Receptor
US-09-773-877B-24

  Query Match             84.9%;  Score 2069.5;  DB 4;  Length 455;
  Best Local Similarity   85.7%;  Pred. No. 1e-165;
  Matches  395;  Conservative   16;  Mismatches   41;  Indels    9;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
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Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              |||||||||: | |   :|| ||||||||||   | | |: |:|:||  : :  | |
Db        118 HRQTNTIIDIQLLPRKSLELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPER 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
                  |: :|:    | |||  |:: | | | | |::|:   : || | |||    ||||||
Db        178 RSQQTHTELS---SILTIHNVSQHDLGSYVCKANNGIQRFRESTEVIVHENGPGDKTHTC 234

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 294

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 354

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 414

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        415 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 455


RESULT 5
US-09-773-877B-18
; Sequence 18, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1(2-3)-Fc (Mut3)
US-09-773-877B-18

  Query Match             84.1%;  Score 2049;  DB 4;  Length 462;
  Best Local Similarity   84.2%;  Pred. No. 5.6e-164;
  Matches  393;  Conservative   13;  Mismatches   47;  Indels   14;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              |||||||||| :|    ::|  |  ||||||| | ||  :   | ||   |::   :  |
Db        118 HRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRR- 176

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK--------- 231
                || |    | | |||| :   |:|||||   ||    |  :| | :::|
Db        177 -IDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSC 235

Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 295

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 355

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 415

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        416 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462


RESULT 6
US-09-773-877B-16
; Sequence 16, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 452
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1(2-3 deltaB)-Fc
US-09-773-877B-16

  Query Match             83.6%;  Score 2038;  DB 4;  Length 452;
  Best Local Similarity   83.9%;  Pred. No. 4.6e-163;
  Matches  392;  Conservative   10;  Mismatches   41;  Indels   24;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              |||||||||| :|    ::|  |  ||||||| | ||  :   | ||              |
Db        118 HRQTNTIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYP-----------D 165

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK--------- 231
                || |    | | |||| :   |:|||||   ||    |  :| | :::|
Db        166 EIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSC 225

Qy        232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 285

Qy        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 345

Qy        352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 405

Qy        412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        406 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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RESULT 7
US-09-773-877B-20
; Sequence 20, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 567
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1(1-3 R->N)-Fc (Mut4)
US-09-773-877B-20

  Query Match             82.7%;  Score 2015.5;  DB 4;  Length 567;
  Best Local Similarity   69.6%;  Pred. No. 4.9e-161;
  Matches  396;  Conservative   14;  Mismatches   46;  Indels  113;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSG---------------------------------- 26
              ||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK 60

Qy         27 ------------------------------------------------------------ 26

Db         61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET 120

Qy         27 --------SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 78
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 180

Qy         79 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI 138
              |||||||||||||||||||||||||||||||||||||||||||||||||||| :|    :
Db        181 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV 240

Qy        139 ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
              :|  |  |||||| | ||  :   | ||  |::  :  |    || |    | | |||
Db        241 KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKNASVRRR--IDQSNSHANIFYSVLTI 298

Qy        199 DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---------DKTHTCPPCPAPELLGGP 249
              | :   |:|||||   ||   |  :| | :::|         ||||||||||||||||||
Db        299 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 358

Qy        250 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418

Qy        310 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 478

Qy        370 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538

Qy        430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              ||||||||||||||||||||||||||||
Db        539 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567


RESULT 8
US-09-773-877B-12
; Sequence 12, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 567
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt(1-3)-Fc
US-09-773-877B-12

  Query Match             82.7%;  Score 2014.5;  DB 4;  Length 567;
  Best Local Similarity   69.6%;  Pred. No. 6e-161;
  Matches  396;  Conservative   13;  Mismatches   47;  Indels  113;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSG---------------------------------- 26
              ||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK 60

Qy         27 ------------------------------------------------------------ 26

Db         61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET 120

Qy         27 --------SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 78
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 180

Qy         79 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI 138
              |||||||||||||||||||||||||||||||||||||||||||||||||||| :|    :
Db        181 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV 240

Qy        139 ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
              :|  |  |||||| | ||  :   | ||  |::  :  |    || |    | | |||
Db        241 KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRR--IDQSNSHANIFYSVLTI 298

Qy        199 DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---------DKTHTCPPCPAPELLGGP 249
              | :   |:|||||   ||   |  :| | :::|         ||||||||||||||||||
Db        299 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 358

Qy        250 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418

Qy        310 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 478

Qy        370 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538

Qy        430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              ||||||||||||||||||||||||||||
Db        539 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567


RESULT 9
US-09-773-877B-14
; Sequence 14, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877B
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 557
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Flt1(1-3 deltaB)-Fc (Mut1)
US-09-773-877B-14

  Query Match             82.2%;  Score 2003.5;  DB 4;  Length 557;
  Best Local Similarity   69.4%;  Pred. No. 4.9e-160;
  Matches  395;  Conservative   10;  Mismatches   41;  Indels  123;  Gaps    3;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSG---------------------------------- 26
              ||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHK 60

Qy         27 ------------------------------------------------------------ 26

Db         61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET 120

Qy         27 --------SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 78
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 180

Qy         79 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| :|    :
Db        181 GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV 240

Qy        139 ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
              :|  |  ||||||| | ||  :   | ||             |   || |    | | |||
Db        241 KLLRGHTLVLNCTATTPLNTRVQMTWSYP-----------DEIDQSNSHANIFYSVLTI 288

Qy        199 DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---------DKTHTCPPCPAPELLGGP 249
              | :   |:|||||   ||   |  :| | :::|         ||||||||||||||||||
Db        289 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 348

Qy        250 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 408

Qy        310 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 468

Qy        370 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 528

Qy        430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              ||||||||||||||||||||||||||||
Db        529 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 557


RESULT 10
US-08-227-496C-15
; Sequence 15, Application US/08227496C
; Patent No. 6130202
;  GENERAL INFORMATION:
;    APPLICANT:  Greve, Jeffrey M.
;    APPLICANT:  McClelland, Alan
;    TITLE OF INVENTION:  Multimeric Forms of Human
;    TITLE OF INVENTION:  Rhinovirus Receptor Protein
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bayer Corporation
;      STREET:  400 Morgan Lane
;      CITY:  West Haven
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06516
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  diskette, 1.44 Mb storage
;      COMPUTER:  Dell OptiPlex GX1
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/227,496C
;      FILING DATE:  04/14/94
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/903,069
;      FILING DATE:  06/22/92
;      APPLICATION NUMBER:  07/704,984
;      FILING DATE:  05/24/91
;      APPLICATION NUMBER:  07/556,238
;      FILING DATE:  07/20/90
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barbara A. Shimei
;      REGISTRATION NUMBER:  29,862
;      REFERENCE/DOCKET NUMBER:  MTI 214.2C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 812-2786
;      TELEFAX:  (203) 812-5492
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  680 amino acid residues
;      TYPE:  amino acids
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  protein
;    HYPOTHETICAL:  no
;    FRAGMENT TYPE:  complete sequence
;    FEATURE:
;      NAME/KEY:  tICAM(185)/IgG fusion protein
;      OTHER INFORMATION:  amino acid residues 1-453 =
;      OTHER INFORMATION:  tICAM(453); amino acid residues 454-680 = amino
;      OTHER INFORMATION:  acid residues 216-442 of human IgG1 heavy chain
US-08-227-496C-15

  Query Match             53.5%;  Score 1304;  DB 3;  Length 680;
  Best Local Similarity   60.6%;  Pred. No. 4.4e-101;
  Matches  281;  Conservative   30;  Mismatches   89;  Indels   64;  Gaps   15;

Qy         15 LSCLLLTGSSSGSDTGRPFVEMYS-EIPEII----HMTEGRELVIPCRVTSPNITVTLKK 69
              |:| :: |: |         | :||   | :|     ::|| |: : |    |   |||
Db        261 LTCAVILGNQSQETL--QTVTIYSFPAPNVILTKPEVSEGTEVTVKCE-AHPRAKVTLNG 317

Qy         70 FPLDTLIPDGKRIIWDSRKGFIISNATYKEIG-LLTCEATVNGHLYKTNYLTHRQTNTII 128
                |  | |          :  ::  || :: |   :| ||    |      | |:     :
Db        318 VPAQPLGP----------RAQLLLKATPEDNGRSFSCSAT----LEVAGQLIHKNQTREL 363

Qy        129 DVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSE 188
              |:  |       : |:   :|          || :| :  |          |:
Db        364 RVLYGP------RLDER---DCPG----------NWTWPENSQQTP-------MCQAWGN 397

Qy        189 MKKFLSTLTIDG----------VTRSDQGLYTCAASS--GLMTKKNSTFV-RVHEKDKT 234
                  |  |  ||           |||  :| | | | |  | :|:| : |     :|||
Db        398 PLPELKCLK-DGTFPLPIGESVTVTRDLEGTYLCRARSTQGEVTRKVTVNVLSPRYEDKT 456

Qy        235 HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 516

Qy        295 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 576

Qy        355 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 636

Qy        415 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||
Db        637 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 680


RESULT 11
US-09-499-846-6
; Sequence 6, Application US/09499846
; Patent No. 6656728
```

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; GENERAL INFORMATION:
;  APPLICANT: Kavanaugh et al.
;  TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
;  TITLE OF INVENTION:  RECEPTOR-IMMUNOGLOBULIN FUSION
;  FILE REFERENCE: 035784/195012 (5784-
;  CURRENT APPLICATION NUMBER: US/09/499,846
;  CURRENT FILING DATE:  2000-02-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-499-846-6

  Query Match            52.5%;  Score 1280;  DB 4;  Length 497;
  Best Local Similarity  54.3%;  Pred. No. 2.9e-99;
  Matches  284;  Conservative   32;  Mismatches  109;  Indels   98;  Gaps   12;

Qy          5 WDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVT----- 59
              |   :    |::  | |  | :   :| |  |   ||     | :  :|   |
Db          4 WKCLLFWAVLVTATLCTARPSPTLPEQP-VAPYWTSPE---KMEKKLHAVPAAKTVKFKC 59

Qy         60 ----SPNITVTLKKFPLDTLIPDGKRIIWDSR-KGFIISNATYKEI---------GLLTC 105
                  :|| |:   |        :||    | |  |: :  ||:  |         |  ||
Db         60 PSSGTPNPTLRWLK--------NGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTC 111

Qy        106 -----EATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGI 160
                   ::| | |:           :|||    |   | |    |       |   :
Db        112 IVENEYGSIN-HTYQ-----------LDVVERSPHRPILQAG----LPANKTVALGSNV 154

Qy        161 DFNWEYPSSKHQHKKLVN----------------RDLKTQSGSEMKKFLSTLTIDGVTR 203
              :|  :  |    | : :                : |||   :   | :  | :  |:
Db        155 EFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSF 214

Qy        204 SDQGLYTCAASSGLMTKKNSTFVRVHEK---------------------------DKTH 235
               | | |||  | : :    :| :: | |                           ||||
Db        215 EDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLEGSGSPGLQEPKSCDKTH 274

Qy        236 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 334

Qy        296 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 394

Qy        356 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 454

Qy        416 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||||
Db        455 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 497


RESULT 12
US-09-499-846-2
; Sequence 2, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
;  APPLICANT: Kavanaugh et al.
;  TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
;  TITLE OF INVENTION:  RECEPTOR-IMMUNOGLOBULIN FUSION
;  FILE REFERENCE: 035784/195012 (5784-
;  CURRENT APPLICATION NUMBER: US/09/499,846
;  CURRENT FILING DATE:  2000-02-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 622
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-499-846-2

  Query Match            52.5%;  Score 1279.5;  DB 4;  Length 622;
  Best Local Similarity  51.2%;  Pred. No. 4.5e-99;
  Matches  287;  Conservative   34;  Mismatches  100;  Indels  139;  Gaps   13;

Qy          6 DTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIP-------EIIHMTEGREL------ 52
              |:|:  |        :| | |||||     | :  :|       :    :| :|
Db         95 DSGLYAC-------VTSSPSGSDTTYFSVNVSDALPSSEDDDDDDDSSSEEKETDNTKPN 147

Qy         53 -----------------VIPCRVT---------SPNITVTLKKFPLDTLIPDGKRIIWDS 86
                              :|   |         :|| |:   |        :||    |
Db        148 PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK--------NGKEFKPDH 199

Qy         87 R-KGFIISNATYKEI---------GLLTC-----EATVNGHLYKTNYLTHRQTNTIIDVV 131
              |  |: :  ||:  |         |  ||       ::| | |:            :|||
Db        200 RIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSIN-HTYQ-----------LDVV 246

Qy        132 LSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVN------------- 178
                  |   | |    |         |   ::|  :  |    | : :
Db        247 ERSPHRPILQAG----LPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 302

Qy        179 ----RDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK--- 231
                  : |||   :   | :  | :  |:  | | ||| | : :    :| :: | |
Db        303 LPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEE 362

Qy        232 --------------------------------DKTHTCPPCPAPELLGGPSVFLFPPKP 258
                                             ||||||||||||||||||||||||||||
Db        363 RPAVMTSPLYLESRGGLVPRGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP 422

Qy        259 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 482

Qy        319 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 542

Qy        379 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 602

Qy        439 MHEALHNHYTQKSLSLSPGK 458
              ||||||||||||||||||||
Db        603 MHEALHNHYTQKSLSLSPGK 622


RESULT 13
US-09-313-942-28
; Sequence 28, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
;  APPLICANT: REGENERON PHARMACEUTICALS, INC.
;  TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
;  TITLE OF INVENTION:  AND USING
;  FILE REFERENCE: REG 203-A
;  CURRENT APPLICATION NUMBER: US/09/313,942
;  CURRENT FILING DATE:  1999-05-19
;  PRIOR APPLICATION NUMBER: 09/313,942
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: 60/101,858
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 28
;   LENGTH: 910
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-313-942-28

  Query Match            52.3%;  Score 1275.5;  DB 4;  Length 910;
  Best Local Similarity  63.5%;  Pred. No. 1.7e-98;
  Matches  257;  Conservative   42;  Mismatches   77;  Indels   29;  Gaps    9;
```

```
Qy          78 DGKRIIWDS------RKGFIISNATYKEIGLLTCEA--TVNGHLYK----TNYLTHRQTN 125
               | | :: |:      :   |: |   |  | || |  |  |       ::|  :
Db         511 DCKPLLLDNIHFSGVKDRLIVMNVAEKHRGNYTCHASYTYLGKQYPITRVIEFITLEENK 570

Qy         126 TIIDVVLSPSH-GIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQ 184
                    |::||::  :|: :| :: | |    :|:    : |   |   :   ::  |  :
Db         571 PTRPVIVSPANETMEVDLGSQIQLICNVTGQLSDIAYWKWN-GSVIDEDDPVLGEDYYSV 629

Qy         185 SGSEMKKFLSTLTIDGVTRSDQGLY----TCAASS--GLMTKKNSTFVRV-----HEKDK 233
                  |:  : :|:  ::  :   |    || | :  |:    :: ::::     :  ||
Db         630 ENPANKRRSTLITVLNISEIESRFYKHPFTCFAKNTHGI----DAAYIQLIYPVTNSGDK 685

Qy         234 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 293
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         686 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 745

Qy         294 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 353
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         746 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 805

Qy         354 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 413
               ||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||||||
Db         806 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 865

Qy         414 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
               |||||||||||||||||||||||||||||||||||||||||||||
Db         866 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 910
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RESULT 14
US-09-499-846-4
; Sequence 4, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-4

Query Match 52.3%; Score 1274.5; DB 4; Length 525;
Best Local Similarity 59.0%; Pred. No. 9.2e-99;
Matches 271; Conservative 25; Mismatches 78; Indels 85; Gaps 9;

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Qy          60 SPNITVTLKKFPLDTLIPDGKRIIWDSR-KGFIISNATYKEI---------GLLTC---- 105
               :|| |:   |        :||    | |  |: :  ||:  |         |  ||
Db          92 TPNPTLRWLK--------NGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVEN 143

Qy         106 -EATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNW 164
                ::| | |:           :|||    |   | |    |       |   ::|
Db         144 EYGSIN-HTYQ-----------LDVVERSPHRPILQAG----LPANKTVALGSNVEFMC 186

Qy         165 EYPSSKHQHKKLVN-----------------RDLKTQSGSEMKKFLSTLTIDGVTRSDQG 207
               :  |    | : :               : |||   :   | :  | :  |:  | |
Db         187 KVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAG 246

Qy         208 LYTCAASSGLMTKKNSTFVRVHEK--------------------------DKTHTCPP 239
                ||| | : :    :| :: | |                          ||||||||
Db         247 EYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLEGSGSPGLQEPKSCDKTHTCPP 306

Qy         240 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 299
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         307 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 366

Qy         300 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 359
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         367 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 426

Qy         360 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 419
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         427 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 486

Qy         420 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
               |||||||||||||||||||||||||||||||||||||||
Db         487 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 525
```

RESULT 15
US-09-499-846-12
; Sequence 12, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-12

Query Match 52.1%; Score 1269.5; DB 4; Length 488;
Best Local Similarity 54.9%; Pred. No. 2.2e-98;
Matches 282; Conservative 32; Mismatches 111; Indels 89; Gaps 12;

```
Qy           5 WDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVT----- 59
               |   :    |::  | |   | :  :| |  |   ||     | :  :|   |
Db           4 WKCLLFWAVLVTATLCTARPSPTLPEQP-VAPYWTSPE---KMEKKLHAVPAAKTVKFKC 59

Qy          60 ----SPNITVTLKKFPLDTLIPDGKRIIWDSR-KGFIISNATYKEI---------GLLTC 105
                   :|| |:   |        :||    | |  |: :  ||:  |         |  ||
Db          60 PSSGTPNPTLRWLK--------NGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTC 111

Qy         106 -----EATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGI 160
                    ::| | |:           :|||    |   | |    |       |   :
Db         112 IVENEYGSIN-HTYQ-----------LDVVERSPHRPILQAG----LPANKTVALGSNV 154

Qy         161 DFNWEYPSSKHQHKKLVN-----------------RDLKTQSGSEMKKFLSTLTIDGVTR 203
               :|  :  |    | : :               : |||   :   | :  | :  |:
Db         155 EFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSF 214

Qy         204 SDQGLYTCAASSGLMTKKNSTFVRVHEK-------------------DKTHTCPPCPAPE 244
                | | ||| | : :    :| :: | |                   ||||||||||||
Db         215 EDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLEPKSCDKTHTCPPCPAPE 274

Qy         245 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 304
               | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         275 LEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 334

Qy         305 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 364
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         335 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPP 394

Qy         365 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 424
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         395 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 454

Qy         425 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
               |||||||||||||||||||||||||||||||||
Db         455 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 488
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Search completed: September 23, 2005, 17:18:51
Job time : 48 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 23, 2005, 17:12:57 ; Search time 123 Seconds
(without alignments)
1515.541 Million cell updates/sec

Title: US-10-811-170-2
Perfect score: 2437
Sequence: 1 MVSYWDTGVLLCALLSCLLL.....MHEALHNHYTQKSLSLSPGK 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2437	100.0	458	10	US-09-773-877A-26	Sequence 26, Appl
2	2437	100.0	458	15	US-10-609-775-10	Sequence 10, Appl
3	2437	100.0	458	16	US-10-860-958-2	Sequence 2, Appli
4	2437	100.0	458	17	US-10-830-902-2	Sequence 2, Appli
5	2437	100.0	458	17	US-10-897-802-2	Sequence 2, Appli
6	2437	100.0	458	17	US-10-880-021-10	Sequence 10, Appl
7	2437	100.0	458	17	US-10-909-011-4	Sequence 4, Appli
8	2437	100.0	458	18	US-10-988-243-16	Sequence 16, Appl
9	2437	100.0	458	18	US-10-998-881-4	Sequence 4, Appli
10	2437	100.0	458	20	US-11-016-097-16	Sequence 16, Appl
11	2437	100.0	458	20	US-11-039-144-2	Sequence 2, Appli
12	2399	98.4	458	10	US-09-773-877A-22	Sequence 22, Appl
13	2399	98.4	458	15	US-10-609-775-8	Sequence 8, Appli
14	2399	98.4	458	17	US-10-880-021-8	Sequence 8, Appli
15	2399	98.4	458	17	US-10-909-011-2	Sequence 2, Appli
16	2399	98.4	458	18	US-10-988-243-12	Sequence 12, Appl
17	2399	98.4	458	18	US-10-998-881-2	Sequence 2, Appli
18	2399	98.4	458	20	US-11-016-097-12	Sequence 12, Appl
19	2384	97.8	458	17	US-10-855-559-13	Sequence 13, Appl
20	2297	94.3	432	16	US-10-846-477A-16	Sequence 16, Appl
21	2261	92.8	431	10	US-09-773-877A-27	Sequence 27, Appl
22	2256.5	92.6	430	20	US-11-016-097-17	Sequence 17, Appl
23	2203	90.4	434	17	US-10-880-021-29	Sequence 29, Appl
24	2069.5	84.9	455	10	US-09-773-877A-24	Sequence 24, Appl
25	2069.5	84.9	455	15	US-10-609-775-13	Sequence 13, Appl
26	2069.5	84.9	455	17	US-10-880-021-13	Sequence 13, Appl
27	2069.5	84.9	455	18	US-10-988-243-14	Sequence 14, Appl
28	2069.5	84.9	455	20	US-11-016-097-14	Sequence 14, Appl
29	2049	84.1	462	10	US-09-773-877A-18	Sequence 18, Appl
30	2049	84.1	462	18	US-10-988-243-8	Sequence 8, Appli
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32	2038	83.6	452	10	US-09-773-877A-16	Sequence 16, Appl
33	2038	83.6	452	18	US-10-988-243-6	Sequence 6, Appli
34	2038	83.6	452	20	US-11-016-097-6	Sequence 6, Appli
35	2015.5	82.7	567	10	US-09-773-877A-20	Sequence 20, Appl
36	2015.5	82.7	567	18	US-10-988-243-10	Sequence 10, Appl
37	2015.5	82.7	567	20	US-11-016-097-10	Sequence 10, Appl
38	2014.5	82.7	567	10	US-09-773-877A-12	Sequence 12, Appl
39	2014.5	82.7	567	18	US-10-988-243-2	Sequence 2, Appli
40	2014.5	82.7	567	20	US-11-016-097-2	Sequence 2, Appli
41	2003.5	82.2	557	10	US-09-773-877A-14	Sequence 14, Appl
42	2003.5	82.2	557	18	US-10-988-243-4	Sequence 4, Appli
43	2003.5	82.2	557	20	US-11-016-097-4	Sequence 4, Appli
44	1726.5	70.8	934	14	US-10-232-838-17	Sequence 17, Appl
45	1716	70.4	949	14	US-10-232-838-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-773-877A-26
; Sequence 26, Application US/09773877A
; Publication No. US20030017977A1
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877A
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VEGFR1R2-FcdeltaC1(a) Receptor
US-09-773-877A-26

Query Match 100.0%; Score 2437; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
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Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
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Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
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Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458

Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 2
US-10-609-775-10
; Sequence 10, Application US/10609775
; Publication No. US20040014667A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas J. Daly
;  APPLICANT:  James P. Fandl
;  APPLICANT:  Nicholas J. Papadopoulos
;  TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: REG 710D
;  CURRENT APPLICATION NUMBER: US/10/609,775
;  CURRENT FILING DATE:  2003-06-30
;  PRIOR APPLICATION NUMBER: 10/009,852
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: PCT/US00/14142
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/138,133
;  PRIOR FILING DATE: 1999-06-08
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-609-775-10

  Query Match            100.0%;  Score 2437;  DB 15;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-152;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

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Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458

Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 3
US-10-860-958-2
; Sequence 2, Application US/10860958
; Publication No. US20040265309A1
; GENERAL INFORMATION:
;  APPLICANT: Kandel, Jessica
;  APPLICANT:  Holash, Jocelyn
;  APPLICANT:  Yamashiro, Darrell
;  APPLICANT:  Huang, Jianzhong
;  APPLICANT:  Yancopoulos, George
;  APPLICANT:  Rudge, John
;  TITLE OF INVENTION: Method of Tumor Regression with VEGF
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: REG 714A
;  CURRENT APPLICATION NUMBER: US/10/860,958
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: 60/476,425
;  PRIOR FILING DATE: 2003-06-06
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-860-958-2

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  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

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Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

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Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458

Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 4
US-10-830-902-2
; Sequence 2, Application US/10830902
; Publication No. US20050004027A1
; GENERAL INFORMATION:
;  APPLICANT: Stanley Wiegand
;  APPLICANT:  Jingtai Cao
;  APPLICANT:  Claus Cursiefien
;  TITLE OF INVENTION: Method of Treating Corneal Transplant
;  TITLE OF INVENTION:  Rejection
;  FILE REFERENCE: REG 713B
;  CURRENT APPLICATION NUMBER: US/10/830,902
;  CURRENT FILING DATE:  2004-04-23
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-830-902-2

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  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
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Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
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Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
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Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
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Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
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Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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RESULT 5
US-10-897-802-2
; Sequence 2, Application US/10897802
; Publication No. US20050032699A1
; GENERAL INFORMATION:
;  APPLICANT: Jocelyn Holash
;  APPLICANT:  Robert Jaffe
;  APPLICANT:  Limin Hu
;  APPLICANT:  George D. Yancopoulos
;  TITLE OF INVENTION: Composition of a VEGF Antagonist and an Anti-Proliferative Agent
;  FILE REFERENCE: REG 715B
;  CURRENT APPLICATION NUMBER: US/10/897,802
;  CURRENT FILING DATE:  2004-07-23
;  PRIOR APPLICATION NUMBER: 60/493,971
;  PRIOR FILING DATE: 2003-08-08
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-897-802-2

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  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
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Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
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Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
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Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
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Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
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Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
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Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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RESULT 6
US-10-880-021-10
; Sequence 10, Application US/10880021
; Publication No. US20050043236A1
; GENERAL INFORMATION:
;  APPLICANT: Daly, thomas J.
;  APPLICANT:  Fandl, James P.
;  APPLICANT:  Papadopoulos, Nicholas J.
;  TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof
;  FILE REFERENCE: RGE 710D2
;  CURRENT APPLICATION NUMBER: US/10/880,021
;  CURRENT FILING DATE:  2004-06-29
;  PRIOR APPLICATION NUMBER: 10/609,775
;  PRIOR FILING DATE: 2003-06-30
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-880-021-10

  Query Match            100.0%;  Score 2437;  DB 17;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-152;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
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Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||
Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 7
US-10-909-011-4
; Sequence 4, Application US/10909011
; Publication No. US20050112061A1
; GENERAL INFORMATION:
;  APPLICANT: Jocelyn Holash
;  APPLICANT:  George Yancopoulos
;  APPLICANT:  Phyllis R. Wachsberger
;  APPLICANT:  Adam P. Dicker
;  APPLICANT:  Randy Burd
;  TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
;  FILE REFERENCE: REG 716A
;  CURRENT APPLICATION NUMBER: US/10/909,011
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: 60/492,864
;  PRIOR FILING DATE: 2003-08-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-909-011-4

  Query Match            100.0%;  Score 2437;  DB 17;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-152;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||
Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 8
US-10-988-243-16
; Sequence 16, Application US/10988243
; Publication No. US20050175610A1
; GENERAL INFORMATION:
;  APPLICANT: Wiegand, Stanley
;  APPLICANT:  Papadopoulos, Nicholas J.
;  APPLICANT:  Yancopoulos, George
;  TITLE OF INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinectic Prop
;  TITLE OF INVENTION:  and Methods of Making and Using Thereof
;  FILE REFERENCE: REG 710F
;  CURRENT APPLICATION NUMBER: US/10/988,243
;  CURRENT FILING DATE:  2004-11-12
;  PRIOR APPLICATION NUMBER: 10/009,852
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: PCT/US00/14142
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/138,133
;  PRIOR FILING DATE: 1999-06-08
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-988-243-16

  Query Match            100.0%;  Score 2437;  DB 18;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-152;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
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Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||
Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 9
US-10-998-881-4
; Sequence 4, Application US/10998881
; Publication No. US20050196340A1
; GENERAL INFORMATION:
;  APPLICANT: Jocelyn Holash
;  APPLICANT:  George Yancopoulos
;  APPLICANT:  Phyllis R. Wachsberger
;  APPLICANT:  Adam P. Dicker
;  APPLICANT:  Randy Burd
;  TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
;  FILE REFERENCE: 716B
;  CURRENT APPLICATION NUMBER: US/10/998,881
;  CURRENT FILING DATE:  2004-11-29
;  PRIOR APPLICATION NUMBER: 10/909,011
;  PRIOR FILING DATE: 2004-07-30
;  PRIOR APPLICATION NUMBER: 60/492,864
;  PRIOR FILING DATE: 2003-08-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-998-881-4

  Query Match             100.0%;  Score 2437;  DB 18;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-152;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||
Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 10
US-11-016-097-16
; Sequence 16, Application US/11016097
; Publication No. US20050163798A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas J. Papadopoulos et al.
;  TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
;  TITLE OF INVENTION:  PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
;  TITLE OF INVENTION:  AND USING THEREOF
;  FILE REFERENCE: REG 710-A-US
;  CURRENT APPLICATION NUMBER: US/11/016,097
;  CURRENT FILING DATE:  2004-12-17
;  PRIOR APPLICATION NUMBER: US/10/009,852
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: PCT/US00/14142
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/138,133
;  PRIOR FILING DATE: 1999-06-08
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-016-097-16

  Query Match             100.0%;  Score 2437;  DB 20;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-152;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||
Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 11
US-11-039-144-2
; Sequence 2, Application US/11039144
; Publication No. US20050197291A1
; GENERAL INFORMATION:
;  APPLICANT: Stanley Wiegand
;  APPLICANT:  Jingtai Cao
```

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;  APPLICANT:  Claus Cursiefien
;  TITLE OF INVENTION: Method of Treating Corneal Transplant
;  TITLE OF INVENTION:  Rejection In High Risk Keratoplasty Patients
;  FILE REFERENCE: 713C
;  CURRENT APPLICATION NUMBER: US/11/039,144
;  CURRENT FILING DATE:  2005-01-19
;  PRIOR APPLICATION NUMBER: 10/830,902
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: 60/473,734
;  PRIOR FILING DATE: 2003-05-28
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-039-144-2

  Query Match           100.0%;  Score 2437;  DB 20;  Length 458;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-152;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240

Qy        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300

Qy        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360

Qy        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

Qy        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||
Db        421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 12
US-09-773-877A-22
; Sequence 22, Application US/09773877A
; Publication No. US20030017977A1
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877A
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1D2.Flk1D3.FcdeltaC1(a) Receptor
US-09-773-877A-22

  Query Match           98.4%;  Score 2399;  DB 10;  Length 458;
  Best Local Similarity  98.7%;  Pred. No. 1.1e-149;
  Matches  455;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    2;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        178 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC 237

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458


RESULT 13
US-10-609-775-8
; Sequence 8, Application US/10609775
; Publication No. US20040014667A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas J. Daly
;  APPLICANT:  James P. Fandl
;  APPLICANT:  Nicholas J. Papadopoulos
;  TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: REG 710D
;  CURRENT APPLICATION NUMBER: US/10/609,775
;  CURRENT FILING DATE:  2003-06-30
;  PRIOR APPLICATION NUMBER: 10/009,852
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: PCT/US00/14142
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/138,133
;  PRIOR FILING DATE: 1999-06-08
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-609-775-8

  Query Match           98.4%;  Score 2399;  DB 15;  Length 458;
  Best Local Similarity  98.7%;  Pred. No. 1.1e-149;
  Matches  455;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    2;

Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57
```

```
Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        178 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC 237

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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RESULT 14
US-10-880-021-8
; Sequence 8, Application US/10880021
; Publication No. US20050043236A1
; GENERAL INFORMATION:
; APPLICANT: Daly, thomas J.
; APPLICANT: Fandl, James P.
; APPLICANT: Papadopoulos, Nicholas J.
; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof
; FILE REFERENCE: RGE 710D2
; CURRENT APPLICATION NUMBER: US/10/880,021
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/609,775
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 458
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-880-021-8

Query Match 98.4%; Score 2399; DB 17; Length 458;
Best Local Similarity 98.7%; Pred. No. 1.1e-149;
Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

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Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        178 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC 237

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
```

RESULT 15
US-10-909-011-2
; Sequence 2, Application US/10909011
; Publication No. US20050112061A1
; GENERAL INFORMATION:
; APPLICANT: Jocelyn Holash
; APPLICANT: George Yancopoulos
; APPLICANT: Phyllis R. Wachsberger
; APPLICANT: Adam P. Dicker
; APPLICANT: Randy Burd
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
; FILE REFERENCE: REG 716A
; CURRENT APPLICATION NUMBER: US/10/909,011
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/492,864
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 458
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-909-011-2

Query Match 98.4%; Score 2399; DB 17; Length 458;
Best Local Similarity 98.7%; Pred. No. 1.1e-149;
Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

```
Qy          1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57

Qy         61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117

Qy        121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 177

Qy        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        178 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC 237

Qy        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297

Qy        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357

Qy        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417

Qy        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
              |||||||||||||||||||||||||||||||||||||||||
Db        418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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Db 418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458

Search completed: September 23, 2005, 17:21:05
Job time : 125 secs

10/811,170

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup)** that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.